

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lal, Preeti
Hillman, Jennifer L.
Corley, Neil C.
Guegler, Karl J.
Baugh, Mariah
Sather, Susan
Shah, Purvi

(ii) TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS

(iii) NUMBER OF SEQUENCES: 154

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
(B) STREET: 3174 PORTER DRIVE
(C) CITY: PALO ALTO
(D) STATE: CALIFORNIA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: TO BE ASSIGNED
(B) FILING DATE: HEREWITH
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: BILLINGS, LUCY J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0459 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650) 855-0555
(B) TELEFAX: (650) 845-4166

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: HEARNOT01
 (B) CLONE: 305841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 :

Met Ala Ala Thr Leu Gly Pro Leu Gly Ser Trp Gln Gln Trp Arg
 5 10 15
 Arg Cys Leu Ser Ala Arg Asp Gly Ser Arg Met Leu Leu Leu Leu
 20 25 30
 Leu Leu Leu Gly Ser Gly Gln Gly Pro Gln Gln Val Gly Ala Gly
 35 40 45
 Gln Thr Phe Glu Tyr Leu Lys Arg Glu His Ser Leu Ser Lys Pro
 50 55 60
 Tyr Gln Gly Val Gly Thr Gly Ser Ser Ser Leu Trp Asn Leu Met
 65 70 75
 Gly Asn Ala Met Val Met Thr Gln Tyr Ile Arg Leu Thr Pro Asp
 80 85 90
 Met Gln Ser Lys Gln Gly Ala Leu Trp Asn Arg Val Pro Cys Phe
 95 100 105
 Leu Arg Asp Trp Glu Leu Gln Val His Phe Lys Ile His Gly Gln
 110 115 120
 Gly Lys Lys Asn Leu His Gly Asp Gly Leu Ala Ile Trp Tyr Thr
 125 130 135
 Lys Asp Arg Met Gln Pro Gly Pro Val Phe Gly Asn Met Asp Lys
 140 145 150
 Phe Val Gly Leu Gly Val Phe Val Asp Thr Tyr Pro Asn Glu Glu
 155 160 165
 Lys Gln Gln Glu Arg Val Phe Pro Tyr Ile Ser Ala Met Val Asn
 170 175 180
 Asn Gly Ser Leu Ser Tyr Asp His Glu Arg Asp Gly Arg Pro Thr
 185 190 195
 Glu Leu Gly Gly Cys Thr Ala Ile Val Arg Asn Leu His Tyr Asp
 200 205 210
 Thr Phe Leu Val Ile Arg Tyr Val Lys Arg His Leu Thr Ile Met
 215 220 225
 Met Asp Ile Asp Gly Lys His Glu Trp Arg Asp Cys Ile Glu Val
 230 235 240
 Pro Gly Val Arg Leu Pro Arg Gly Tyr Tyr Phe Gly Thr Ser Ser
 245 250 255
 Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys
 260 265 270
 Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu Lys Leu
 275 280 285
 His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met Lys Leu Pro
 290 295 300
 Glu Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe
 305 310 315
 Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val
 320 325 330
 Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys
 335 340 345
 Arg Phe Tyr

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 194 amino acids
 (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: EOSIHET02
 - (B) CLONE: 322866

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2 :

Met	Gly	Met	Ser	Ser	Leu	Lys	Leu	Leu	Lys	Tyr	Val	Leu	Phe	Phe
5						10							15	
Phe	Asn	Leu	Leu	Phe	Trp	Ile	Cys	Gly	Cys	Cys	Ile	Leu	Gly	Phe
						20			25					30
Gly	Ile	Tyr	Leu	Leu	Ile	His	Asn	Asn	Phe	Gly	Val	Leu	Phe	His
						35			40					45
Asn	Leu	Pro	Ser	Leu	Thr	Leu	Gly	Asn	Val	Phe	Val	Ile	Val	Gly
						50			55					60
Ser	Ile	Ile	Met	Val	Val	Ala	Phe	Leu	Gly	Cys	Met	Gly	Ser	Ile
						65			70					75
Lys	Glu	Asn	Lys	Cys	Leu	Leu	Met	Ser	Phe	Phe	Ile	Leu	Leu	Leu
						80			85					90
Ile	Ile	Leu	Leu	Ala	Glu	Val	Thr	Leu	Ala	Ile	Leu	Leu	Phe	Val
						95			100					105
Tyr	Glu	Gln	Lys	Leu	Asn	Glu	Tyr	Val	Ala	Lys	Gly	Leu	Thr	Asp
						110			115					120
Ser	Ile	His	Arg	Tyr	His	Ser	Asp	Asn	Ser	Thr	Lys	Ala	Ala	Trp
						125			130					135
Asp	Ser	Ile	Gln	Ser	Phe	Leu	Gln	Cys	Cys	Gly	Ile	Asn	Gly	Thr
						140			145					150
Ser	Asp	Leu	Asp	Ser	Gly	Ser	Pro	Ala	Ser	Cys	Pro	Ser	Asp	Arg
						155			160					165
Lys	Val	Glu	Gly	Cys	Tyr	Ala	Lys	Glu	Asp	Phe	Gly	Phe	Ile	Gln
						170			175					180
Phe	Pro	Val	Tyr	Arg	Asn	His	His	His	Leu	Cys	Met	Cys	Asp	
						185			190					

- (2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: BEPINOT01
 - (B) CLONE: 546656

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3 :

Met	Ser	Leu	His	Gly	Lys	Arg	Lys	Glu	Ile	Tyr	Lys	Tyr	Glu	Ala
5						10							15	
Pro	Trp	Thr	Val	Tyr	Ala	Met	Asn	Trp	Ser	Val	Arg	Pro	Asp	Lys
						20			25					30
Arg	Phe	Arg	Leu	Ala	Leu	Gly	Ser	Phe	Val	Glu	Glu	Tyr	Asn	Asn
						35			40					45
Lys	Val	Gln	Leu	Val	Gly	Leu	Asp	Glu	Glu	Ser	Ser	Glu	Phe	Ile
						50			55					60

Cys	Arg	Asn	Thr	Phe	Asp	His	Pro	Tyr	Pro	Thr	Thr	Lys	Leu	Met
				65					70					75
Trp	Ile	Pro	Asp	Thr	Lys	Gly	Val	Tyr	Pro	Asp	Leu	Leu	Ala	Thr
				80					85					90
Ser	Gly	Asp	Tyr	Leu	Arg	Val	Trp	Arg	Val	Gly	Glu	Thr	Glu	Thr
				95					100					105
Arg	Leu	Glu	Cys	Leu	Leu	Asn	Asn	Asn	Lys	Asn	Ser	Asp	Phe	Cys
				110					115					120
Ala	Pro	Leu	Thr	Ser	Phe	Asp	Trp	Asn	Glu	Val	Asp	Pro	Tyr	Leu
				125					130					135
Leu	Gly	Thr	Ser	Ser	Ile	Asp	Thr	Thr	Cys	Thr	Ile	Trp	Gly	Leu
				140					145					150
Glu	Thr	Gly	Gln	Val	Leu	Gly	Arg	Val	Asn	Leu	Val	Ser	Gly	His
				155					160					165
Val	Lys	Thr	Gln	Leu	Ile	Ala	His	Asp	Lys	Glu	Val	Tyr	Asp	Ile
				170					175					180
Ala	Phe	Ser	Arg	Ala	Gly	Gly	Gly	Arg	Asp	Met	Phe	Ala	Ser	Val
				185					190					195
Gly	Ala	Asp	Gly	Ser	Val	Arg	Met	Phe	Asp	Leu	Arg	His	Leu	Glu
				200					205					210
His	Ser	Thr	Ile	Ile	Tyr	Glu	Asp	Pro	Gln	His	His	Pro	Leu	Leu
				215					220					225
Arg	Leu	Cys	Trp	Asn	Lys	Gln	Asp	Pro	Asn	Tyr	Leu	Ala	Thr	Met
				230					235					240
Ala	Met	Asp	Gly	Met	Glu	Val	Val	Ile	Leu	Asp	Val	Arg	Val	Pro
				245					250					255
Cys	Thr	Pro	Val	Ala	Arg	Leu	Asn	Asn	His	Arg	Ala	Cys	Val	Asn
				260					265					270
Gly	Ile	Ala	Trp	Ala	Pro	His	Ser	Ser	Cys	His	Ile	Cys	Thr	Ala
				275					280					285
Ala	Asp	Asp	His	Gln	Ala	Leu	Ile	Trp	Asp	Ile	Gln	Gln	Met	Pro
				290					295					300
Arg	Ala	Ile	Glu	Asp	Pro	Ile	Leu	Ala	Tyr	Thr	Ala	Glu	Gly	Glu
				305					310					315
Ile	Asn	Asn	Val	Gln	Trp	Ala	Ser	Thr	Gln	Pro	Asp	Trp	Ile	Ala
				320					325					330
Ile	Cys	Tyr	Asn	Asn	Cys	Leu	Glu	Ile	Leu	Arg	Val			
				335					340					

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SYNORAT03
- (B) CLONE: 693453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4 :

Met	Glu	Glu	Leu	Asp	Gly	Glu	Pro	Thr	Val	Thr	Leu	Ile	Pro	Gly
				5					10					15
Val	Asn	Ser	Lys	Lys	Asn	Gln	Met	Tyr	Phe	Asp	Trp	Gly	Pro	Gly
				20					25					30
Glu	Met	Leu	Val	Cys	Glu	Thr	Ser	Phe	Asn	Lys	Lys	Glu	Lys	Ser

	35	40	45											
Glu	Met	Val	Pro	Ser	Cys	Pro	Phe	Ile	Tyr	Ile	Ile	Arg	Lys	Asp
	50								55					60
Val	Asp	Val	Tyr	Ser	Gln	Ile	Leu	Arg	Lys	Leu	Phe	Asn	Glu	Ser
	65								70					75
His	Gly	Ile	Phe	Leu	Gly	Leu	Gln	Arg	Ile	Asp	Glu	Glu	Leu	Thr
	80								85					90
Gly	Lys	Ser	Arg	Lys	Ser	Gln	Leu	Val	Arg	Val	Ser	Lys	Asn	Tyr
	95								100					105
Arg	Ser	Val	Ile	Arg	Ala	Cys	Met	Glu	Glu	Met	His	Gln	Val	Ala
	110								115					120
Ile	Ala	Ala	Lys	Asp	Pro	Ala	Asn	Gly	Arg	Gln	Phe	Ser	Ser	Gln
	125								130					135
Val	Ser	Ile	Leu	Ser	Ala	Met	Glu	Leu	Ile	Trp	Asn	Leu	Cys	Glu
	140								145					150
Ile	Leu	Phe	Ile	Glu	Val	Ala	Pro	Ala	Gly	Pro	Leu	Leu	Leu	His
	155								160					165
Leu	Leu	Asp	Trp	Val	Arg	Leu	His	Val	Cys	Glu	Val	Asp	Ser	Leu
	170								175					180
Ser	Ala	Asp	Val	Leu	Gly	Ser	Glu	Asn	Pro	Ser	Lys	His	Asp	Ser
	185								190					195
Phe	Trp	Asn	Leu	Val	Thr	Ile	Leu	Val	Leu	Gln	Gly	Arg	Leu	Asp
	200								205					210
Glu	Ala	Arg	Gln	Met	Leu	Ser	Lys	Glu	Ala	Asp	Ala	Ser	Pro	Ala
	215								220					225
Ser	Ala	Gly	Ile	Cys	Arg	Ile	Met	Gly	Asp	Leu	Met	Arg	Thr	Met
	230								235					240
Pro	Ile	Leu	Ser	Pro	Gly	Asn	Thr	Gln	Thr	Leu	Thr	Glu	Leu	Glu
	245								250					255
Leu	Lys	Trp	Gln	His	Trp	His	Glu	Glu	Cys	Glu	Arg	Tyr	Leu	Gln
	260								265					270
Asp	Ser	Thr	Phe	Ala	Thr	Ser	Pro	His	Leu	Glu	Ser	Leu	Leu	Lys
	275								280					285
Ile	Met	Leu	Gly	Asp	Glu	Ala	Ala	Leu	Leu	Glu	Gln	Lys	Glu	Leu
	290								295					300
Leu	Ser	Asn	Trp	Tyr	His	Phe	Leu	Val	Thr	Arg	Leu	Leu	Tyr	Ser
	305								310					315
Asn	Pro	Thr	Val	Lys	Pro	Ile	Asp	Leu	His	Tyr	Tyr	Ala	Gln	Ser
	320								325					330
Ser	Leu	Asp	Leu	Phe	Leu	Gly	Gly	Glu	Ser	Ser	Pro	Glu	Pro	Leu
	335								340					345
Asp	Asn	Ile	Leu	Leu	Leu	Ala	Ala	Phe	Asp	Ile	His	Gln	Val	
	350								355					360
Ile	Lys	Glu	Cys	Ser	Ile	Ala	Leu	Ser	Asn	Trp	Trp	Phe	Val	Ala
	365								370					375
His	Leu	Thr	Asp	Leu	Leu	Asp	His	Cys	Lys	Leu	Leu	Gln	Ser	His
	380								385					390
Asn	Leu	Tyr	Phe	Gly	Ser	Asn	Met	Arg	Glu	Phe	Leu	Leu	Glu	
	395								400					405
Tyr	Ala	Ser	Gly	Leu	Phe	Ala	His	Pro	Ser	Leu	Trp	Gln	Leu	Gly
	410								415					420
Val	Asp	Tyr	Phe	Asp	Tyr	Cys	Pro	Glu	Leu	Gly	Arg	Val	Ser	Leu
	425								430					435
Glu	Leu	His	Ile	Glu	Arg	Ile	Pro	Leu	Asn	Thr	Glu	Gln	Lys	Ala
	440								445					450
Leu	Lys	Val	Leu	Arg	Ile	Cys	Glu	Gln	Arg	Gln	Met	Thr	Glu	Gln
	455								460					465
Val	Arg	Ser	Ile	Cys	Lys	Ile	Leu	Ala	Met	Lys	Ala	Val	Arg	Asn
	470								475					480
Asn	Arg	Leu	Gly	Ser	Ala	Leu	Ser	Trp	Ser	Ile	Arg	Ala	Lys	Asp
	485								490					495

Ala	Ala	Phe	Ala	Thr	Leu	Val	Ser	Asp	Arg	Phe	Leu	Arg	Asp	Tyr
				500					505					510
Cys	Glu	Arg	Gly	Cys	Phe	Ser	Asp	Leu	Asp	Leu	Ile	Asp	Asn	Leu
				515					520					525
Gly	Pro	Ala	Met	Met	Leu	Ser	Asp	Arg	Leu	Thr	Phe	Leu	Gly	Lys
				530					535					540
Tyr	Arg	Glu	Phe	His	Arg	Met	Tyr	Gly	Glu	Lys	Arg	Phe	Ala	Asp
				545					550					555
Ala	Ala	Ser	Leu	Leu	Leu	Ser	Leu	Met	Thr	Ser	Arg	Ile	Ala	Pro
				560					565					570
Arg	Ser	Phe	Trp	Met	Thr	Leu	Leu	Thr	Asp	Ala	Leu	Pro	Leu	Leu
				575					580					585
Glu	Gln	Lys	Gln	Val	Ile	Phe	Ser	Ala	Glu	Gln	Thr	Tyr	Glu	Leu
				590					595					600
Met	Arg	Cys	Leu	Glu	Asp	Leu	Thr	Ser	Arg	Arg	Pro	Val	His	Gly
				605					610					615
Glu	Ser	Asp	Thr	Glu	Gln	Leu	Gln	Asp	Asp	Asp	Ile	Glu	Thr	Thr
				620					625					630
Lys	Val	Glu	Met	Leu	Arg	Leu	Ser	Leu	Ala	Arg	Asn	Leu	Ala	Arg
				635					640					645
Ala	Ile	Ile	Arg	Glu	Gly	Ser	Leu	Glu	Gly	Ser				
				650					655					

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT03
- (B) CLONE: 866885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5 :

Met	Ala	Pro	Asp	Pro	Trp	Phe	Ser	Thr	Tyr	Asp	Ser	Thr	Cys	Gln
					5				10					15
Ile	Ala	Gln	Glu	Ile	Ala	Glu	Lys	Ile	Gln	Gln	Arg	Asn	Gln	Tyr
					20				25					30
Glu	Arg	Lys	Gly	Glu	Lys	Ala	Pro	Lys	Leu	Thr	Val	Thr	Ile	Arg
					35				40					45
Ala	Leu	Leu	Gln	Asn	Leu	Lys	Glu	Lys	Ile	Ala	Leu	Leu	Lys	Asp
					50				55					60
Leu	Leu	Leu	Arg	Ala	Val	Ser	Thr	His	Gln	Ile	Thr	Gln	Leu	Glu
					65				70					75
Gly	Asp	Arg	Arg	Gln	Asn	Leu	Leu	Asp	Asp	Leu	Val	Thr	Arg	Glu
					80				85					90
Arg	Leu	Leu	Leu	Ala	Ser	Phe	Lys	Asn	Glu	Gly	Ala	Glu	Pro	Asp
					95				100					105
Leu	Ile	Arg	Ser	Ser	Leu	Met	Ser	Glu	Glu	Ala	Lys	Arg	Gly	Ala
					110				115					120
Pro	Asn	Pro	Trp	Leu	Phe	Glu	Glu	Pro	Glu	Glu	Thr	Arg	Gly	Leu
					125				130					135
Gly	Phe	Asp	Glu	Ile	Arg	Gln	Gln	Gln	Gln	Lys	Ile	Ile	Gln	Glu
					140				145					150
Gln	Asp	Ala	Gly	Leu	Asp	Ala	Leu	Ser	Ser	Ile	Ile	Ser	Arg	Gln

	155	160	165											
Lys	Gln	Met	Gly	Gln	Glu	Ile	Gly	Asn	Glu	Leu	Asp	Glu	Gln	Asn
	170				175					180				
Glu	Ile	Ile	Asp	Asp	Leu	Ala	Asn	Leu	Val	Glu	Asn	Thr	Asp	Glu
	185						190			195				
Lys	Leu	Arg	Asn	Glu	Thr	Arg	Arg	Val	Asn	Met	Val	Asp	Arg	Lys
	200						205			210				
Ser	Ala	Ser	Cys	Gly	Met	Ile	Met	Val	Ile	Leu	Leu	Leu	Leu	Val
	215						220			225				
Ala	Ile	Val	Val	Val	Ala	Val	Trp	Pro	Thr	Asn				
	230						235							

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: LUNGNOT03
 - (B) CLONE: 1242271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6 :

Met	Leu	Leu	Asp	Thr	Val	Gln	Lys	Val	Phe	Gln	Lys	Met	Leu	Glu
					5					10				15
Cys	Ile	Ala	Arg	Ser	Phe	Arg	Lys	Gln	Pro	Glu	Glu	Gly	Leu	Arg
						20				25				30
Leu	Leu	Tyr	Ser	Val	Gln	Arg	Pro	Leu	His	Glu	Phe	Ile	Thr	Ala
						35				40				45
Val	Gln	Ser	Arg	His	Thr	Asp	Thr	Pro	Val	His	Arg	Gly	Val	Leu
						50				55				60
Ser	Thr	Leu	Ile	Ala	Gly	Pro	Val	Val	Glu	Ile	Ser	His	Gln	Leu
						65				70				75
Arg	Lys	Val	Ser	Asp	Val	Glu	Glu	Leu	Thr	Pro	Pro	Glu	His	Leu
						80				85				90
Ser	Asp	Leu	Pro	Pro	Phe	Ser	Arg	Cys	Leu	Ile	Gly	Ile	Ile	Ile
						95				100				105
Lys	Ser	Ser	Asn	Val	Val	Arg	Ser	Phe	Leu	Asp	Glu	Leu	Lys	Ala
						110				115				120
Cys	Val	Ala	Ser	Asn	Asp	Ile	Glu	Gly	Ile	Val	Cys	Leu	Thr	Ala
						125				130				135
Ala	Val	His	Ile	Ile	Leu	Val	Ile	Asn	Ala	Gly	Lys	His	Lys	Ser
						140				145				150
Ser	Lys	Val	Arg	Glu	Val	Ala	Ala	Thr	Val	His	Arg	Lys	Leu	Lys
						155				160				165
Thr	Phe	Met	Glu	Ile	Thr	Leu	Glu	Glu	Asp	Ser	Ile	Glu	Arg	Phe
						170				175				180
Leu	Tyr	Glu	Ser	Ser	Ser	Arg	Thr	Leu	Gly	Glu	Leu	Leu	Asn	Ser
						185				190				195

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 608 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: LUNGFET03
 (B) CLONE: 1255027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7 :

Met	Thr	Lys	Thr	Asp	Glu	Thr	Thr	Leu	Val	Ala	Ser	Trp	Glu	Thr
														15
5														
Arg	Glu	Lys	Thr	Ala	Lys	Thr	Thr	Leu	Phe	Leu	Pro	Leu	Glu	Phe
														30
20														
Trp	Ser	Tyr	Lys	Ala	Glu	Val	Pro	His	Leu	Pro	Glu	Leu	Ala	Tyr
														45
35														
Ser	Ala	Arg	Ser	Lys	Met	Ala	Glu	Leu	Asn	Thr	His	Val	Asn	Val
														60
50														
Lys	Glu	Lys	Ile	Tyr	Ala	Val	Arg	Ser	Val	Val	Pro	Asn	Lys	Ser
														75
65														
Asn	Asn	Glu	Ile	Val	Leu	Val	Leu	Gln	Gln	Phe	Asp	Phe	Asn	Val
														90
80														
Asp	Lys	Ala	Val	Gln	Ala	Phe	Val	Asp	Gly	Ser	Ala	Ile	Gln	Val
														105
95														
Leu	Lys	Glu	Trp	Asn	Met	Thr	Gly	Lys	Lys	Lys	Asn	Asn	Lys	Arg
														120
110														
Lys	Arg	Ser	Lys	Ser	Lys	Gln	His	Gln	Gly	Asn	Lys	Asp	Ala	Lys
														135
125														
Asp	Lys	Val	Glu	Arg	Pro	Glu	Ala	Gly	Pro	Leu	Gln	Pro	Gln	Pro
														150
140														
Pro	Gln	Ile	Gln	Asn	Gly	Pro	Met	Asn	Gly	Cys	Glu	Lys	Asp	Ser
														165
155														
Ser	Ser	Thr	Asp	Ser	Ala	Asn	Glu	Lys	Pro	Ala	Leu	Ile	Pro	Arg
														180
170														
Glu	Lys	Lys	Ile	Ser	Ile	Leu	Glu	Glu	Pro	Ser	Lys	Ala	Leu	Arg
														195
185														
Gly	Val	Thr	Glu	Gly	Asn	Arg	Leu	Leu	Gln	Gln	Lys	Leu	Ser	Leu
														210
200														
Asp	Gly	Asn	Pro	Lys	Pro	Ile	His	Gly	Thr	Thr	Glu	Arg	Ser	Asp
														225
215														
Gly	Leu	Gln	Trp	Ser	Ala	Glu	Gln	Pro	Cys	Asn	Pro	Ser	Lys	Pro
														240
230														
Lys	Ala	Lys	Thr	Ser	Pro	Val	Lys	Ser	Asn	Thr	Pro	Ala	Ala	His
														255
245														
Leu	Glu	Ile	Lys	Pro	Asp	Glu	Leu	Ala	Lys	Lys	Arg	Gly	Pro	Asn
														270
260														
Ile	Glu	Lys	Ser	Val	Lys	Asp	Leu	Gln	Arg	Cys	Thr	Val	Ser	Leu
														285
275														
Thr	Arg	Tyr	Arg	Val	Met	Ile	Lys	Glu	Glu	Val	Asp	Ser	Ser	Val
														300
290														
Lys	Lys	Ile	Lys	Ala	Ala	Phe	Ala	Glu	Leu	His	Asn	Cys	Ile	Ile
														315
305														
Asp	Lys	Glu	Val	Ser	Leu	Met	Ala	Glu	Met	Asp	Lys	Val	Lys	Glu
														330
320														
Glu	Ala	Met	Glu	Ile	Leu	Thr	Ala	Arg	Gln	Lys	Lys	Ala	Glu	Glu
														345
335														
340														

Leu Lys Arg Leu Thr Asp Leu Ala Ser Gln Met Ala Glu Met Gln
 350 355 360
 Leu Ala Glu Leu Arg Ala Glu Ile Lys His Phe Val Ser Glu Arg
 365 370 375
 Lys Tyr Asp Glu Glu Leu Gly Lys Ala Ala Arg Phe Ser Cys Asp
 380 385 390
 Ile Glu Gln Leu Lys Ala Gln Ile Met Leu Cys Gly Glu Ile Thr
 395 400 405
 His Pro Lys Asn Asn Tyr Ser Ser Arg Thr Pro Cys Ser Ser Leu
 410 415 420
 Leu Pro Leu Leu Asn Ala His Ala Ala Thr Ser Gly Lys Gln Ser
 425 430 435
 Asn Phe Ser Arg Lys Ser Ser Thr His Asn Lys Pro Ser Glu Gly
 440 445 450
 Lys Ala Ala Asn Pro Lys Met Val Ser Ser Leu Pro Ser Thr Ala
 455 460 465
 Asp Pro Ser His Gln Thr Met Pro Ala Asn Lys Gln Asn Gly Ser
 470 475 480
 Ser Asn Gln Arg Arg Phe Asn Pro Gln Tyr His Asn Asn Arg
 485 490 495
 Leu Asn Gly Pro Ala Lys Ser Gln Gly Ser Gly Asn Glu Ala Glu
 500 505 510
 Pro Leu Gly Lys Gly Asn Ser Arg His Glu His Arg Arg Gln Pro
 515 520 525
 His Asn Gly Phe Arg Pro Lys Asn Lys Gly Gly Ala Lys Asn Gln
 530 535 540
 Glu Ala Ser Leu Gly Met Lys Thr Pro Glu Ala Pro Ala His Ser
 545 550 555
 Glu Lys Pro Arg Arg Arg Gln His Ala Ala Asp Thr Ser Glu Ala
 560 565 570
 Arg Pro Phe Arg Gly Ser Val Gly Arg Val Ser Gln Cys Asn Leu
 575 580 585
 Cys Pro Thr Arg Ile Glu Val Ser Thr Asp Ala Ala Val Leu Ser
 590 595 600
 Val Pro Ala Val Thr Leu Val Ala
 605

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: TESTTUT02
 - (B) CLONE: 1273453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8 :

Met Val Ile Ser Trp His Leu Ala Ser Asp Met Asp Cys Val Val
 5 10 15
 Thr Leu Thr Thr Asp Ala Ala Arg Arg Ile Tyr Asp Glu Thr Gln
 20 25 30
 Gly Arg Gln Gln Val Leu Pro Leu Asp Ser Ile Tyr Lys Lys Thr
 35 40 45
 Leu Pro Asp Trp Lys Arg Ser Leu Pro His Phe Arg Asn Gly Lys

50	55	60												
Leu	Tyr	Phe	Lys	Pro	Ile	Gly	Asp	Pro	Val	Phe	Ala	Arg	Asp	Leu
65														75
Leu	Thr	Phe	Pro	Asp	Asn	Val	Glu	His	Cys	Glu	Thr	Val	Phe	Gly
80														90
Met	Leu	Leu	Gly	Asp	Thr	Ile	Ile	Leu	Asp	Asn	Leu	Asp	Ala	Ala
95														105
Asn	His	Tyr	Arg	Lys	Glu	Val	Val	Lys	Ile	Thr	His	Cys	Pro	Thr
110														120
Leu	Leu	Thr	Arg	Asp	Gly	Asp	Arg	Ile	Arg	Ser	Asn	Gly	Lys	Phe
125														135
Gly	Gly	Leu	Gln	Asn	Lys	Ala	Pro	Pro	Met	Asp	Lys	Leu	Arg	Gly
140														150
Met	Val	Phe	Gly	Ala	Pro	Val	Pro	Lys	Gln	Cys	Leu	Ile	Leu	Gly
155														165
Glu	Gln	Ile	Asp	Leu	Leu	Gln	Gln	Tyr	Arg	Ser	Ala	Val	Cys	Lys
170														180
Leu	Asp	Ser	Val	Asn	Lys	Asp	Leu	Asn	Ser	Gln	Leu	Glu	Tyr	Leu
185														195
Arg	Thr	Pro	Asp	Met	Arg	Lys	Lys	Lys	Gln	Glu	Leu	Asp	Glu	His
200														210
Glu	Lys	Asn	Leu	Lys	Leu	Ile	Glu	Glu	Lys	Leu	Gly	Met	Thr	Pro
215														225
Ile	Arg	Lys	Cys	Asn	Asp	Ser	Leu	Arg	His	Ser	Pro	Lys	Val	Glu
230														240
Thr	Thr	Asp	Cys	Pro	Val	Pro	Pro	Lys	Arg	Met	Arg	Arg	Glu	Ala
245														255
Thr	Arg	Gln	Asn	Arg	Ile	Ile	Thr	Lys	Thr	Asp	Val			
260														265

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 285 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: TESTTUT02
 - (B) CLONE: 1275261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9 :

Met	Val	Met	Arg	Pro	Leu	Trp	Ser	Leu	Leu	Trp	Glu	Ala	Leu	
5													15	
Leu	Pro	Ile	Thr	Val	Thr	Gly	Ala	Gln	Val	Leu	Ser	Lys	Val	Gly
20														30
Gly	Ser	Val	Leu	Leu	Val	Ala	Ala	Arg	Pro	Pro	Gly	Phe	Gln	Val
35														45
Arg	Glu	Ala	Ile	Trp	Arg	Ser	Leu	Trp	Pro	Ser	Glu	Glu	Leu	Leu
50														60
Ala	Thr	Phe	Arg	Gly	Ser	Leu	Glu	Thr	Leu	Tyr	His	Ser	Arg	
65														75
Phe	Leu	Gly	Arg	Ala	Gln	Leu	His	Ser	Asn	Leu	Ser	Leu	Glu	Leu
80														90
Gly	Pro	Leu	Glu	Ser	Gly	Asp	Ser	Gly	Asn	Phe	Ser	Val	Leu	Met
95														105

Val	Asp	Thr	Arg	Gly	Gln	Pro	Trp	Thr	Gln	Thr	Leu	Gln	Leu	Lys
				110					115					120
Val	Tyr	Asp	Ala	Val	Pro	Arg	Pro	Val	Val	Gln	Val	Phe	Ile	Ala
				125					130					135
Val	Glu	Arg	Asp	Ala	Gln	Pro	Ser	Lys	Thr	Cys	Gln	Val	Phe	Leu
				140					145					150
Ser	Cys	Trp	Ala	Pro	Asn	Ile	Ser	Glu	Ile	Thr	Tyr	Ser	Trp	Arg
				155					160					165
Arg	Glu	Thr	Thr	Met	Asp	Phe	Gly	Met	Glu	Pro	His	Ser	Leu	Phe
				170					175					180
Thr	Asp	Gly	Gln	Val	Leu	Ser	Ile	Ser	Leu	Gly	Pro	Gly	Asp	Arg
				185					190					195
Asp	Val	Ala	Tyr	Ser	Cys	Ile	Val	Ser	Asn	Pro	Val	Ser	Trp	Asp
				200					205					210
Leu	Ala	Thr	Val	Thr	Pro	Trp	Asp	Ser	Cys	His	His	Glu	Ala	Ala
				215					220					225
Pro	Gly	Lys	Ala	Ser	Tyr	Lys	Asp	Val	Leu	Leu	Val	Val	Val	Pro
				230					235					240
Val	Ser	Leu	Leu	Leu	Met	Leu	Val	Thr	Leu	Phe	Ser	Ala	Trp	His
				245					250					255
Trp	Cys	Pro	Cys	Ser	Gly	Lys	Lys	Lys	Lys	Asp	Val	His	Ala	Asp
				260					265					270
Arg	Val	Gly	Pro	Glu	Thr	Glu	Asn	Pro	Leu	Val	Gln	Asp	Leu	Pro
				275					280					285

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT16
- (B) CLONE: 1281682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10 :

Met	Pro	Phe	Thr	Arg	Pro	Leu	Lys	His	Phe	Val	Ser	Leu	Leu	His
						5			10					15
Pro	Ser	Ala	Ser	Gln	Val	His	Asn	Ala	Gly	Gln	His	Gln	Lys	Leu
						20			25					30
Lys	Thr	Leu	Glu	Lys	Ala	Cys	Gly	Leu	Ala	Leu	Gly	Glu	Gly	Arg
						35			40					45
Glu	Gln	Asn	Leu	Cys	Thr	Ser	Leu	Phe	Asn	Leu	Glu	Ile	Arg	His
						50			55					60
Pro	Arg	Asp	Ala	Ile	Ile	Phe	Cys	Val	Ser	Ile	Val	Val	Pro	Leu
						65			70					75

Ser

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: BRSTNOT07
 - (B) CLONE: 1298305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11 :

Met	Thr	Ala	Ser	Thr	Gly	His	Leu	Gly	Leu	Gly	Trp	Ser	Ala	Arg
							5		10					15
Pro	Cys	Pro	Cys	Gly	Thr	Leu	Gly	Ser	Cys	Phe	Leu	Ser	Leu	Phe
							20		25					30
Ala	Ala	Leu	Leu	Trp	Leu	Ala	Ala	Ala	Val	Leu	Gln	Ala	Cys	Val
							35		40					45
Gly	His	Ser	Asp	Glu	Gly	Cys	Gly	Ala	Ser	Gln	Cys	Arg	Arg	Ala
				50					55					60
Ala	Leu	Gly	Ile	Val	Pro	Ser	Pro	Val	Ser	Val	Leu	Arg	Thr	Tyr
				65					70					75
Pro	Gly	Leu	His	His	Gln	Asp	Pro	Val	Phe	Gly	Phe	Arg	Arg	Pro
					80				85					90
Ser	Met	Gly	Lys	Thr	Arg	His	Gln	Pro	Leu	Gln	Gln	Trp	Val	Pro
					95				100					105
Leu	Ala	Cys	Gly	His	Gln	Leu	Gly	Asp	Pro	Gly	Ser	Gly	Pro	Leu
					110				115					120
Leu	Ser	Pro	Val	Ser	Leu	Cys	Cys	Gly	Phe	Trp	Ala	Val	Met	Ser
					125				130					135
Pro	Pro	Leu	Lys	Asp	Val	Phe	Thr	Leu	Thr	Ser	Gly			
					140				145					

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 261 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: LUNGNOT12
 - (B) CLONE: 1360501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12 :

Met	Glu	Leu	Leu	Gln	Val	Thr	Ile	Leu	Phe	Leu	Leu	Pro	Ser	Ile
					5			10						15
Cys	Ser	Ser	Asn	Ser	Thr	Gly	Val	Leu	Glu	Ala	Ala	Asn	Asn	Ser
							20		25					30
Leu	Val	Val	Thr	Thr	Lys	Pro	Ser	Ile	Thr	Thr	Pro	Asn	Thr	
							35		40					45
Glu	Ser	Leu	Gln	Lys	Asn	Val	Val	Thr	Pro	Thr	Thr	Gly	Thr	Thr
					50				55					60
Pro	Lys	Gly	Thr	Ile	Thr	Asn	Glu	Leu	Leu	Lys	Met	Ser	Leu	Met
					65				70					75
Ser	Thr	Ala	Thr	Phe	Leu	Thr	Ser	Lys	Asp	Glu	Gly	Leu	Lys	Ala
					80				85					90

Thr	Thr	Thr	Asp	Val	Arg	Lys	Asn	Asp	Ser	Ile	Ile	Ser	Asn	Val
				95					100					105
Thr	Val	Thr	Ser	Val	Thr	Leu	Pro	Asn	Ala	Val	Ser	Thr	Leu	Gln
				110					115					120
Ser	Ser	Lys	Pro	Lys	Thr	Glu	Thr	Gln	Ser	Ser	Ile	Lys	Thr	Thr
				125					130					135
Glu	Ile	Pro	Gly	Ser	Val	Leu	Gln	Pro	Asp	Ala	Ser	Pro	Ser	Lys
				140					145					150
Thr	Gly	Thr	Leu	Thr	Ser	Ile	Pro	Val	Thr	Ile	Pro	Glu	Asn	Thr
				155					160					165
Ser	Gln	Ser	Gln	Val	Ile	Gly	Thr	Glu	Gly	Gly	Lys	Asn	Ala	Ser
				170					175					180
Thr	Ser	Ala	Thr	Ser	Arg	Ser	Tyr	Ser	Ser	Ile	Ile	Leu	Pro	Val
				185					190					195
Val	Ile	Ala	Leu	Ile	Val	Ile	Thr	Leu	Ser	Val	Phe	Val	Leu	Val
				200					205					210
Gly	Leu	Tyr	Arg	Met	Cys	Trp	Lys	Ala	Asp	Pro	Gly	Thr	Pro	Glu
				215					220					225
Asn	Gly	Asn	Asp	Gln	Pro	Gln	Ser	Asp	Lys	Glu	Ser	Val	Lys	Leu
				230					235					240
Leu	Thr	Val	Lys	Thr	Ile	Ser	His	Glu	Ser	Gly	Glu	His	Ser	Ala
				245					250					255
Gln	Gly	Lys	Thr	Lys	Asn									
				260										

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGNOT12
- (B) CLONE: 1362406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13 :

Met	Ala	Gly	Cys	Pro	Ala	Asp	Arg	Ser	Ile	Leu	Ala	Pro	Leu	Ala
				5					10					15
Trp	Asp	Leu	Gly	Leu	Leu	Leu	Leu	Phe	Val	Gly	Gln	His	Ser	Leu
				20					25					30
Met	Ala	Ala	Glu	Arg	Val	Lys	Ala	Trp	Thr	Ser	Arg	Tyr	Phe	Gly
				35					40					45
Val	Leu	Gln	Arg	Ser	Leu	Tyr	Val	Ala	Cys	Thr	Ala	Leu	Ala	Leu
				50					55					60
Gln	Leu	Val	Met	Arg	Tyr	Trp	Glu	Pro	Ile	Pro	Lys	Gly	Pro	Val
				65					70					75
Leu	Trp	Glu	Ala	Arg	Ala	Glu	Pro	Trp	Ala	Thr	Trp	Val	Pro	Leu
				80					85					90
Leu	Cys	Phe	Val	Leu	His	Val	Ile	Ser	Trp	Leu	Leu	Ile	Phe	Ser
				95					100					105
Ile	Leu	Leu	Val	Phe	Asp	Tyr	Ala	Glu	Leu	Met	Gly	Leu	Lys	Gln
				110					115					120
Val	Tyr	Tyr	His	Val	Leu	Gly	Leu	Gly	Glu	Pro	Leu	Ala	Leu	Lys
				125					130					135
Ser	Pro	Arg	Ala	Leu	Arg	Leu	Phe	Ser	His	Leu	Arg	His	Pro	Val

	140	145	150											
Cys	Val	Glu	Leu	Leu	Thr	Val	Leu	Trp	Val	Val	Pro	Thr	Leu	Gly
	155					160							165	
Thr	Asp	Arg	Leu	Leu	Leu	Ala	Phe	Leu	Leu	Thr	Leu	Tyr	Leu	Gly
	170					175							180	
Leu	Ala	His	Gly	Leu	Asp	Gln	Gln	Asp	Leu	Arg	Tyr	Leu	Arg	Ala
	185					190							195	
Gln	Leu	Gln	Arg	Lys	Leu	His	Leu	Leu	Ser	Arg	Pro	Gln	Asp	Gly
	200					205							210	
Glu	Ala	Glu												

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: LATRTUT02
 - (B) CLONE: 1405329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14 :

Met	Gln	Pro	Arg	Pro	Arg	Gly	Arg	Pro	Pro	Arg	Thr	Arg	Gly	Asp
						5				10			15	
Glu	Ala	Pro	Gln	Trp	His	Leu	Pro	Asp	Ala	Ala	Ala	Leu	Leu	Pro
					20				25				30	
Val	Arg	Leu	Pro	Leu	Ala	Val	Leu	Val	Arg	Gly	Thr	Gln	Arg	Pro
					35				40				45	
Glu	Arg	Arg	Arg	Cys	Gly	Arg	Leu	Pro	Ala	Gly	Val	Pro	Gly	Ala
				50				55					60	
Ala	Arg	Ser	Val	Ala	Arg	Ser								
				65										

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: BRAINOT12
 - (B) CLONE: 1415223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15 :

Met	Leu	Ala	Pro	Gln	Arg	Thr	Arg	Ala	Pro	Ser	Pro	Arg	Ala	Ala
						5				10			15	
Pro	Arg	Pro	Thr	Arg	Ser	Met	Leu	Pro	Ala	Ala	Met	Lys	Gly	Leu
						20				25			30	

Gly	Leu	Ala	Leu	Leu	Ala	Val	Leu	Leu	Cys	Ser	Ala	Pro	Ala	His
														45
									35					40
Gly	Leu	Trp	Cys	Gln	Asp	Cys	Thr	Leu	Thr	Thr	Asn	Ser	Ser	His
														60
									50					55
Cys	Thr	Pro	Lys	Gln	Cys	Gln	Pro	Ser	Asp	Thr	Val	Cys	Ala	Ser
														75
									65					70
Val	Arg	Ile	Thr	Asp	Pro	Ser	Ser	Ser	Arg	Lys	Asp	His	Ser	Val
														90
Asn	Lys	Met	Cys	Ala	Ser	Ser	Cys	Asp	Phe	Val	Lys	Arg	His	Phe
														105
									95					100
Phe	Ser	Asp	Tyr	Leu	Met	Gly	Phe	Ile	Asn	Ser	Gly	Ile	Leu	Lys
														120
									110					115
Val	Asp	Val	Asp	Cys	Cys	Glu	Lys	Asp	Leu	Cys	Asn	Gly	Ala	Ala
														135
									125					130
Gly	Ala	Gly	His	Ser	Pro	Trp	Ala	Leu	Ala	Gly	Gly	Leu	Leu	Leu
														150
Ser	Leu	Gly	Pro	Ala	Leu	Leu	Trp	Ala	Gly	Pro				
														155
														160

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAINOT12
- (B) CLONE: 1416553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16 :

Met	Trp	Ala	Gln	Arg	Val	Leu	Thr	Leu	Trp	Gln	Gly	Leu	Ser	Trp
										5	10			15
Gly	Arg	Pro	Pro	Ser	Gly	Pro	Gly	Ala	Met	Ala	Pro	Arg	Gly	Gln
										20	25			30
Ala	Asp	Leu	Leu	Pro	Ala	Val	Ser	Thr	Pro	Phe	Leu	Ile	Thr	Val
										35	40			45
Trp	Ser	Pro	Ser	Phe	Gly	Cys	Ser	Leu	Arg	Cys	Val	Leu	Gly	Ser
										50	55			60
Ser	Glu	Pro	Glu	Ala	Ser	Phe	Trp	Lys	Pro	Ala	Val	Leu	Pro	Ala
										65	70			75
Pro	Val	Gln	Lys	Pro	Leu	Ser	Pro	Ala	Phe	Pro	Gln	Ala	Gly	Val
										80	85			90
Gly	Val	Gly	Gly	Leu	Cys	Pro	Ser	Ser	Leu	Thr	Leu	Glu	Arg	Trp
										95	100			105
Glu	Ala	Gly	Asn	Leu	His	Leu	Gly	Ala	Trp	Ala	Pro	Pro	Leu	Cys
										110	115			120
Ala	Ser	Gly	Phe	Pro	Ala	Pro	Gly	Arg	Gly	Cys	Ser	Pro	Ser	Trp
										125	130			135
Thr	Pro	Ala	Cys	Pro	Ser									
										140				

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: KIDNNOT09
 - (B) CLONE: 1418517

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17 :

Met	Glu	Asp	Glu	Glu	Val	Ala	Glu	Ser	Trp	Glu	Glu	Ala	Ala	Asp
					5					10				15
Ser	Gly	Glu	Ile	Asp	Arg	Arg	Leu	Glu	Lys	Lys	Leu	Lys	Ile	Thr
					20				25					30
Gln	Lys	Glu	Ser	Arg	Lys	Ser	Lys	Ser	Pro	Pro	Lys	Val	Pro	Ile
					35				40					45
Val	Ile	Gln	Asp	Asp	Ser	Leu	Pro	Ala	Gly	Pro	Pro	Pro	Gln	Ile
					50				55					60
Arg	Ile	Leu	Lys	Arg	Pro	Thr	Ser	Asn	Gly	Val	Val	Ser	Ser	Pro
					65				70					75
Asn	Ser	Thr	Ser	Arg	Pro	Thr	Leu	Pro	Val	Lys	Ser	Leu	Ala	Gln
					80				85					90
Arg	Glu	Ala	Glu	Tyr	Ala	Glu	Ala	Arg	Lys	Arg	Ile	Leu	Gly	Ser
					95				100					105
Ala	Ser	Pro	Glu	Glu	Gln	Glu	Lys	Pro	Ile	Leu	Asp	Arg	Pro	
					110				115					120
Thr	Arg	Ile	Ser	Gln	Pro	Glu	Asp	Ser	Arg	Gln	Pro	Asn	Asn	Val
					125				130					135
Ile	Arg	Gln	Pro	Leu	Gly	Pro	Asp	Gly	Ser	Gln	Gly	Phe	Lys	Gln
					140				145					150
Arg	Arg													

- (2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 742 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: PANCNOT08
 - (B) CLONE: 1438165

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18 :

Met	Ala	Ser	Val	His	Glu	Ser	Leu	Tyr	Phe	Asn	Pro	Met	Met	Thr
					5				10					15
Asn	Gly	Val	Val	His	Ala	Asn	Val	Phe	Gly	Ile	Lys	Asp	Trp	Val
					20				25					30
Thr	Pro	Tyr	Lys	Ile	Ala	Val	Leu	Val	Leu	Leu	Asn	Glu	Met	Ser
					35				40					45
Arg	Thr	Gly	Glu	Gly	Ala	Val	Ser	Leu	Met	Glu	Arg	Arg	Arg	Leu
					50				55					60
Asn	Gln	Leu	Leu	Leu	Pro	Leu	Leu	Gln	Gly	Pro	Asp	Ile	Thr	Leu

65	70	75
Ser Lys Leu Tyr Lys	Leu Ile Glu Glu	Ser Cys Pro Gln Leu Ala
80	85	90
Asn Ser Val Gln Ile Arg Ile Lys	Leu Met Ala Glu Gly Glu	Leu
95	100	105
Lys Asp Met Glu Gln Phe Phe Asp Asp	Leu Ser Asp Ser Phe Ser	
110	115	120
Gly Thr Glu Pro Glu Val His Lys Thr	Ser Val Val Gly Leu Phe	
125	130	135
Leu Arg His Met Ile Leu Ala Tyr Ser	Lys Leu Ser Phe Ser Gln	
140	145	150
Val Phe Lys Leu Tyr Thr Ala Leu Gln	Gln Tyr Phe Gln Asn Gly	
155	160	165
Glu Lys Lys Thr Val Glu Asp Ala Asp	Met Glu Leu Thr Ser Arg	
170	175	180
Asp Glu Gly Glu Arg Lys Met Glu Lys	Glu Glu Leu Asp Val Ser	
185	190	195
Val Arg Glu Glu Glu Val Ser Cys Ser	Gly Pro Leu Ser Gln Lys	
200	205	210
Gln Ala Glu Phe Phe Leu Ser Gln Gln	Ala Ser Leu Leu Lys Asn	
215	220	225
Asp Glu Thr Lys Ala Leu Thr Pro Ala	Ser Leu Gln Lys Glu Leu	
230	235	240
Asn Asn Leu Leu Lys Phe Asn Pro Asp	Phe Ala Glu Ala His Tyr	
245	250	255
Leu Ser Tyr Leu Asn Asn Leu Arg Val	Gln Asp Val Phe Ser Ser	
260	265	270
Thr His Ser Leu Leu His Tyr Phe Asp	Arg Leu Ile Leu Thr Gly	
275	280	285
Ala Glu Ser Lys Ser Asn Gly Glu Glu	Gly Tyr Gly Arg Ser Leu	
290	295	300
Arg Tyr Ala Ala Leu Asn Leu Ala Ala	Leu His Cys Arg Phe Gly	
305	310	315
His Tyr Gln Gln Ala Glu Leu Ala Leu	Gln Glu Ala Ile Arg Ile	
320	325	330
Ala Gln Glu Ser Asn Asp His Val Cys	Leu Gln His Cys Leu Ser	
335	340	345
Trp Leu Tyr Val Leu Gly Gln Lys Arg	Ser Asp Ser Tyr Val Leu	
350	355	360
Leu Glu His Ser Val Lys Lys Ala Val	His Phe Gly Leu Pro Arg	
365	370	375
Ala Phe Ala Gly Lys Thr Ala Asn Lys	Leu Met Asp Ala Leu Lys	
380	385	390
Asp Ser Asp Leu Leu His Trp Lys His	Ser Leu Ser Glu Leu Ile	
395	400	405
Asp Ile Ser Ile Ala Gln Lys Thr Ala	Ile Trp Arg Leu Tyr Gly	
410	415	420
Arg Ser Thr Met Ala Leu Gln Gln Ala	Gln Met Leu Leu Ser Met	
425	430	435
Asn Ser Leu Glu Ala Val Asn Ala Gly	Val Gln Gln Asn Asn Thr	
440	445	450
Glu Ser Phe Ala Val Ala Leu Cys His	Leu Ala Glu Leu His Ala	
455	460	465
Glu Gln Gly Cys Phe Ala Ala Ala Ser	Glu Val Leu Lys His Leu	
470	475	480
Lys Glu Arg Phe Pro Pro Asn Ser Gln	His Ala Gln Leu Trp Met	
485	490	495
Leu Cys Asp Gln Lys Ile Gln Phe Asp	Arg Ala Met Asn Asp Gly	
500	505	510
Lys Tyr His Leu Ala Asp Ser Leu Val	Thr Gly Ile Thr Ala Leu	
515	520	525

Asn	Ser	Ile	Glu	Gly	Val	Tyr	Arg	Lys	Ala	Val	Val	Leu	Gln	Ala
				530				535						540
Gln	Asn	Gln	Met	Ser	Glu	Ala	His	Lys	Leu	Leu	Gln	Lys	Leu	
				545				550						555
Val	His	Cys	Gln	Lys	Leu	Lys	Asn	Thr	Glu	Met	Val	Ile	Ser	Val
				560				565						570
Leu	Leu	Ser	Val	Ala	Glu	Leu	Tyr	Trp	Arg	Ser	Ser	Ser	Pro	Thr
				575				580						585
Ile	Ala	Leu	Pro	Met	Leu	Leu	Gln	Ala	Leu	Ala	Leu	Ser	Lys	Glu
				590				595						600
Tyr	Arg	Leu	Gln	Tyr	Leu	Ala	Ser	Glu	Thr	Val	Leu	Asn	Leu	Ala
				605				610						615
Phe	Ala	Gln	Leu	Ile	Leu	Gly	Ile	Pro	Glu	Gln	Ala	Leu	Ser	Leu
				620				625						630
Leu	His	Met	Ala	Ile	Glu	Pro	Ile	Leu	Ala	Asp	Gly	Ala	Ile	Leu
				635				640						645
Asp	Lys	Gly	Arg	Ala	Met	Phe	Leu	Val	Ala	Lys	Cys	Gln	Val	Ala
				650				655						660
Ser	Ala	Ala	Ser	Tyr	Asp	Gln	Pro	Lys	Lys	Ala	Glu	Ala	Leu	Glu
				665				670						675
Ala	Ala	Ile	Glu	Asn	Leu	Asn	Glu	Ala	Lys	Asn	Tyr	Phe	Ala	Lys
				680				685						690
Val	Asp	Cys	Lys	Glu	Arg	Ile	Arg	Asp	Val	Val	Tyr	Phe	Gln	Ala
				695				700						705
Arg	Leu	Tyr	His	Thr	Leu	Gly	Lys	Thr	Gln	Glu	Arg	Asn	Arg	Cys
				710				715						720
Ala	Met	Leu	Phe	Arg	Gln	Leu	His	Gln	Glu	Leu	Pro	Ser	His	Gly
				725				730						735
Val	Pro	Leu	Ile	Asn	His	Leu								
				740										

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 805 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: THYRNOT03
 - (B) CLONE: 1440381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19 :

Met	Asp	Gly	Ile	Leu	Asp	Glu	Ser	Leu	Leu	Glu	Thr	Cys	Pro	Ile
				5				10						15
Gln	Ser	Pro	Leu	Gln	Val	Phe	Ala	Gly	Met	Gly	Gly	Leu	Ala	Leu
				20				25						30
Ile	Ala	Glu	Arg	Leu	Pro	Met	Leu	Tyr	Pro	Glu	Val	Ile	Gln	Gln
				35				40						45
Val	Ser	Ala	Pro	Val	Val	Thr	Ser	Thr	Thr	Gln	Glu	Lys	Pro	Tyr
				50				55						60
Asp	Ser	Asp	Gln	Phe	Glu	Trp	Val	Thr	Ile	Glu	Gln	Ser	Gly	Glu
				65				70						75
Leu	Val	Tyr	Glu	Ala	Pro	Glu	Thr	Val	Ala	Ala	Glu	Pro	Pro	Pro
				80				85						90
Ile	Lys	Ser	Ala	Val	Gln	Thr	Met	Ser	Pro	Ile	Pro	Ala	His	Ser

	95		100		105									
Leu	Ala	Ala	Phe	Gly	Leu	Phe	Leu	Arg	Leu	Pro	Gly	Tyr	Ala	Glu
					110				115					120
Val	Leu	Leu	Lys	Glu	Arg	Lys	His	Ala	Gln	Cys	Leu	Leu	Arg	Leu
					125				130					135
Val	Leu	Gly	Val	Thr	Asp	Asp	Gly	Glu	Gly	Ser	His	Ile	Leu	Gln
				140					145					150
Ser	Pro	Ser	Ala	Asn	Val	Leu	Pro	Thr	Leu	Pro	Phe	His	Val	Leu
				155					160					165
Arg	Ser	Leu	Phe	Ser	Thr	Thr	Pro	Leu	Thr	Thr	Asp	Asp	Gly	Val
				170					175					180
Leu	Leu	Arg	Arg	Met	Ala	Leu	Glu	Ile	Gly	Ala	Leu	His	Leu	Ile
				185					190					195
Leu	Val	Cys	Leu	Ser	Ala	Leu	Ser	His	His	Ser	Pro	Arg	Val	Pro
				200					205					210
Asn	Ser	Ser	Val	Asn	Gln	Thr	Glu	Pro	Gln	Val	Ser	Ser	Ser	His
				215					220					225
Asn	Pro	Thr	Ser	Thr	Glu	Glu	Gln	Gln	Leu	Tyr	Trp	Ala	Lys	Gly
				230					235					240
Thr	Gly	Phe	Gly	Thr	Gly	Ser	Thr	Ala	Ser	Gly	Trp	Asp	Val	Glu
				245					250					255
Gln	Ala	Leu	Thr	Lys	Gln	Arg	Leu	Glu	Glu	Glu	His	Val	Thr	Cys
				260					265					270
Leu	Leu	Gln	Val	Leu	Ala	Ser	Tyr	Ile	Asn	Pro	Val	Ser	Ser	Ala
				275					280					285
Val	Asn	Gly	Glu	Ala	Gln	Ser	Ser	His	Glu	Thr	Arg	Gly	Gln	Asn
				290					295					300
Ser	Asn	Ala	Leu	Pro	Ser	Val	Leu	Leu	Glu	Leu	Leu	Ser	Gln	Ser
				305					310					315
Cys	Leu	Ile	Pro	Ala	Met	Ser	Ser	Tyr	Leu	Arg	Asn	Asp	Ser	Val
				320					325					330
Leu	Asp	Met	Ala	Arg	His	Val	Pro	Leu	Tyr	Arg	Ala	Leu	Leu	Glu
				335					340					345
Leu	Leu	Arg	Ala	Ile	Ala	Ser	Cys	Ala	Ala	Met	Val	Pro	Leu	Leu
				350					355					360
Leu	Pro	Leu	Ser	Thr	Glu	Asn	Gly	Glu	Glu	Glu	Glu	Gln	Ser	
				365					370					375
Glu	Cys	Gln	Thr	Ser	Val	Gly	Thr	Leu	Leu	Ala	Lys	Met	Lys	Thr
				380					385					390
Cys	Val	Asp	Thr	Tyr	Thr	Asn	Arg	Leu	Arg	Ser	Lys	Arg	Glu	Asn
				395					400					405
Val	Lys	Thr	Gly	Val	Lys	Pro	Asp	Ala	Ser	Asp	Gln	Glu	Pro	Glu
				410					415					420
Gly	Leu	Thr	Leu	Leu	Val	Pro	Asp	Ile	Gln	Lys	Thr	Ala	Glu	Ile
				425					430					435
Val	Tyr	Ala	Ala	Thr	Thr	Ser	Leu	Arg	Gln	Ala	Asn	Gln	Glu	Lys
				440					445					450
Asn	Trp	Val	Asn	Thr	Pro	Arg	Arg	Arg	Leu	Met	Asn	Pro	Lys	Pro
				455					460					465
Leu	Ser	Val	Leu	Lys	Ser	Leu	Glu	Glu	Lys	Tyr	Val	Ala	Val	Met
				470					475					480
Lys	Lys	Leu	Gln	Phe	Asp	Thr	Phe	Glu	Met	Val	Ser	Glu	Asp	Glu
				485					490					495
Asp	Gly	Lys	Leu	Gly	Phe	Lys	Val	Asn	Tyr	His	Tyr	Met	Ser	Gln
				500					505					510
Val	Lys	Asn	Ala	Asn	Asp	Ala	Asn	Ser	Ala	Ala	Arg	Ala	Arg	Arg
				515					520					525
Leu	Ala	Gln	Glu	Ala	Val	Thr	Leu	Ser	Thr	Ser	Leu	Pro	Leu	Ser
				530					535					540
Ser	Ser	Ser	Ser	Val	Phe	Val	Arg	Cys	Asp	Glu	Glu	Arg	Leu	Asp
				545					550					555

Ile	Met	Lys	Val	Leu	Ile	Thr	Gly	Pro	Ala	Asp	Thr	Pro	Tyr	Ala
				560				565						570
Asn	Gly	Cys	Phe	Glu	Phe	Asp	Val	Tyr	Phe	Pro	Gln	Asp	Tyr	Pro
				575				580						585
Ser	Ser	Pro	Pro	Leu	Val	Asn	Leu	Glu	Thr	Thr	Gly	Gly	His	Ser
				590				595						600
Val	Arg	Phe	Asn	Pro	Asn	Leu	Tyr	Asn	Asp	Gly	Lys	Val	Cys	Leu
				605				610						615
Ser	Ile	Leu	Asn	Thr	Trp	His	Gly	Arg	Pro	Glu	Glu	Lys	Trp	Asn
				620				625						630
Pro	Gln	Thr	Ser	Ser	Phe	Leu	Gln	Val	Leu	Val	Ser	Val	Gln	Ser
				635				640						645
Leu	Ile	Leu	Val	Ala	Glu	Pro	Tyr	Phe	Asn	Glu	Pro	Gly	Tyr	Glu
				650				655						660
Arg	Ser	Arg	Gly	Thr	Pro	Ser	Gly	Thr	Gln	Ser	Ser	Arg	Glu	Tyr
				665				670						675
Asp	Gly	Asn	Ile	Arg	Gln	Ala	Thr	Val	Lys	Trp	Ala	Met	Leu	Glu
				680				685						690
Gln	Ile	Arg	Asn	Pro	Ser	Pro	Cys	Phe	Lys	Glu	Val	Ile	His	Lys
				695				700						705
His	Phe	Tyr	Leu	Lys	Arg	Val	Glu	Ile	Met	Ala	Gln	Cys	Glu	Glu
				710				715						720
Trp	Ile	Ala	Asp	Ile	Gln	Gln	Tyr	Ser	Ser	Asp	Lys	Arg	Val	Gly
				725				730						735
Arg	Thr	Met	Ser	His	His	Ala	Ala	Ala	Leu	Lys	Arg	His	Thr	Ala
				740				745						750
Gln	Leu	Arg	Glu	Glu	Leu	Leu	Lys	Leu	Pro	Cys	Pro	Glu	Gly	Leu
				755				760						765
Asp	Pro	Asp	Thr	Asp	Asp	Ala	Pro	Glu	Val	Cys	Arg	Ala	Thr	Thr
				770				775						780
Gly	Ala	Glu	Glu	Thr	Leu	Met	His	Asp	Gln	Val	Lys	Pro	Ser	Ser
				785				790						795
Ser	Lys	Glu	Leu	Pro	Ser	Asp	Phe	Gln	Leu					
				800				805						

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGNOT14
- (B) CLONE: 1510839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20 :

Met	Lys	Ala	Ser	Gln	Cys	Cys	Cys	Cys	Leu	Ser	His	Leu	Leu	Ala
				5					10					15
Ser	Val	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Glu	Leu	Ser	Gly	Pro	Leu
				20					25					30
Ala	Val	Leu	Leu	Gln	Ala	Ala	Glu	Ala	Ala	Pro	Gly	Leu	Gly	Pro
				35				40						45
Pro	Asp	Pro	Arg	Pro	Arg	Thr	Leu	Pro	Pro	Leu	Pro	Pro	Gly	Pro
				50				55						60
Thr	Pro	Ala	Gln	Gln	Pro	Gly	Arg	Gly	Leu	Ala	Glu	Ala	Ala	Gly

65	70	75
Pro Arg Gly Ser Glu	Gly Gly Asn Gly	Ser Asn Pro Val Ala Gly
80	85	90
Leu Glu Thr Asp Asp His	Gly Gly Lys Ala	Gly Glu Gly Ser Val
95	100	105
Gly Gly Gly Leu Ala Val Ser Pro Asn	Pro Gly Asp Lys Pro	Met
110	115	120
Thr Gln Arg Ala Leu Thr Val Leu Met	Val Val Ser Gly Ala	Val
125	130	135
Leu Val Tyr Phe Val Val Arg Thr Val	Arg Met Arg Arg Arg	Asn
140	145	150
Arg Lys Thr Arg Arg Tyr Gly Val Leu	Asp Thr Asn Ile Glu	Asn
155	160	165
Met Glu Leu Thr Pro Leu Glu Gln Asp	Asp Glu Asp Asp Asp	Asn
170	175	180
Thr Leu Phe Asp Ala Asn His Pro Arg	Arg Arg Glu Cys Ala	Phe
185	190	195

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SPLNNNOT04
- (B) CLONE: 1534876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21 :

Met Trp Phe Leu Gly Cys Thr Gly Pro Gly Cys Gly Cys Ala Gly		
5	10	15
Val Cys Lys Val Val Pro Cys Ile Ser Thr Gly Phe Glu Thr Ser		
20	25	30
Gly Pro Cys Pro Ser Ser Arg Glu Gly Phe Leu Phe Phe Leu Thr		
35	40	45
Gln Val Thr Phe Gln Pro Phe Gln Phe Pro Ser Phe Ser Ala Leu		
50	55	60
Pro Ser Asn Ser Ala Asn Pro Gly Val Gly Ser Gln Gly Gly Arg		
65	70	75
Glu Cys Pro Thr Thr Phe Ser Gly Gln Pro Leu Thr Pro Lys Pro		
80	85	90
Leu Pro Pro Ser Ile Leu His Pro Leu Pro Ile Gln Pro Lys Cys		
95	100	105
Pro Gln Leu Gly Leu Ser Cys Ile Pro Val Glu Gly Pro Leu Pro		
110	115	120
Cys Leu Ser Glu Val Arg Leu Cys Cys Val Met Gly Arg Leu Cys		
125	130	135
Pro Ser Pro Pro Leu Ala Arg Cys Thr Cys Phe Leu Val Cys Thr		
140	145	150
Arg Cys Pro Gly Gly Pro Ser Leu Pro Cys Gln		
155	160	

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 160 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: SPLNNNOT04
 - (B) CLONE: 1559131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22 :

Met	Asp	Lys	Leu	Lys	Val	Leu	Ser	Gly	Gln	Asp	Thr	Glu	Asp	
													15	
5								10						
Arg	Ser	Gly	Leu	Ser	Glu	Val	Val	Glu	Ala	Ser	Ser	Leu	Ser	Trp
														30
20								25						
Ser	Thr	Arg	Ile	Lys	Gly	Phe	Ile	Ala	Cys	Phe	Ala	Ile	Gly	Ile
									40					45
35														
Leu	Cys	Ser	Leu	Leu	Gly	Thr	Val	Leu	Leu	Trp	Val	Pro	Arg	Lys
														60
50								55						
Gly	Leu	His	Leu	Phe	Ala	Val	Phe	Tyr	Thr	Phe	Gly	Asn	Ile	Ala
									70					75
65														
Ser	Ile	Gly	Ser	Thr	Ile	Phe	Leu	Met	Gly	Pro	Val	Lys	Gln	Leu
									85					90
80														
Lys	Arg	Met	Phe	Glu	Pro	Thr	Arg	Leu	Ile	Ala	Thr	Ile	Met	Val
									95					105
95										100				
Leu	Leu	Cys	Phe	Ala	Leu	Thr	Leu	Cys	Ser	Ala	Phe	Trp	Trp	His
									110					120
110										115				
Asn	Lys	Gly	Leu	Ala	Leu	Ile	Phe	Cys	Ile	Leu	Gln	Ser	Leu	Ala
									125					135
125										130				
Leu	Thr	Trp	Tyr	Ser	Leu	Ser	Phe	Ile	Pro	Phe	Ala	Arg	Asp	Ala
									140					150
140										145				
Val	Lys	Lys	Cys	Phe	Ala	Val	Cys	Leu	Ala					
									155					
										160				

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: BLADNOT03
 - (B) CLONE: 1601473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23 :

Met	Gln	Ala	Lys	Tyr	Ser	Ser	Thr	Arg	Asp	Met	Leu	Asp	Asp	Asp
										5	10			15
Gly	Asp	Thr	Thr	Met	Ser	Leu	His	Ser	Gln	Ala	Ser	Ala	Thr	Thr
														30
20										25				
Arg	His	Pro	Glu	Pro	Arg	Arg	Thr	Glu	His	Arg	Ala	Pro	Ser	Ser
														45
35										40				
Thr	Trp	Arg	Pro	Val	Ala	Leu	Thr	Leu	Leu	Thr	Leu	Cys	Leu	Val
										50				60
											55			

Leu Leu Ile Gly Leu Ala Ala Leu Gly Leu Leu Cys Lys Ser Ala
 65 70 75
 Leu

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT12
- (B) CLONE: 1615809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24 :

Met Ile Ser Tyr Ile Val Leu Leu Ser Ile Leu Leu Trp Pro Leu
 5 10 15
 Val Val Tyr His Glu Leu Ile Gln Arg Met Tyr Thr Arg Leu Glu
 20 25 30
 Pro Leu Leu Met Gln Leu Asp Tyr Ser Met Lys Ala Glu Ala Asn
 35 40 45
 Ala Leu His His Lys His Asp Lys Arg Lys Arg Gln Gly Lys Asn
 50 55 60
 Ala Pro Pro Gly Gly Asp Glu Pro Leu Ala Glu Thr Glu Ser Glu
 65 70 75
 Ser Glu Ala Glu Leu Ala Gly Phe Ser Pro Val Val Asp Val Lys
 80 85 90
 Lys Thr Ala Leu Ala Leu Ala Ile Thr Asp Ser Glu Leu Ser Asp
 95 100 105
 Glu Glu Ala Ser Ile Leu Glu Ser Gly Gly Phe Ser Val Ser Arg
 110 115 120
 Ala Thr Thr Pro Gln Leu Thr Asp Val Ser Glu Asp Leu Asp Gln
 125 130 135
 Gln Ser Leu Pro Ser Glu Pro Glu Glu Thr Leu Ser Arg Asp Leu
 140 145 150
 Gly Glu Gly Glu Gly Glu Leu Ala Pro Pro Glu Asp Leu Leu
 155 160 165
 Gly Arg Pro Gln Ala Leu Ser Arg Gln Ala Leu Asp Ser Glu Glu
 170 175 180
 Glu Glu Glu Asp Val Ala Ala Lys Glu Thr Leu Leu Arg Leu Ser
 185 190 195
 Ser Pro Leu His Phe Val Asn Thr His Phe Asn Gly Ala Gly Ser
 200 205 210
 Pro Gln Asp Gly Val Lys Cys Ser Pro Gly Gly Pro Val Glu Thr
 215 220 225
 Leu Ser Pro Glu Thr Val Ser Gly Gly Leu Thr Ala Leu Pro Gly
 230 235 240
 Thr Leu Ser Pro Pro Leu Cys Leu Val Gly Ser Asp Pro Ala Pro
 245 250 255
 Ser Pro Ser Ile Leu Pro Pro Val Pro Gln Asp Ser Pro Gln Pro
 260 265 270
 Leu Pro Ala Pro Glu Glu Glu Glu Ala Leu Thr Thr Glu Asp Phe
 275 280 285
 Glu Leu Leu Asp Gln Gly Glu Leu Glu Gln Leu Asn Ala Glu Leu
 290 295 300
 Gly Leu Glu Pro Glu Thr Pro Pro Lys Pro Pro Asp Ala Pro Pro
 305 310 315
 Leu Gly Pro Asp Ile His Ser Leu Val Gln Ser Asp Gln Glu Ala

320	325	330
Gln Ala Val Ala Glu Pro		
335		

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 150 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: COLNOT19
 - (B) CLONE: 1634813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25 :

Met Asn Leu Trp Leu Leu Ala Cys Leu Val Ala Gly Phe Leu Gly	5	10 15
Ala Trp Ala Pro Ala Val His Ala Gln Gly Val Phe Glu Asp Cys	20	25 30
Cys Leu Ala Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg	35	40 45
Ala Trp Thr Tyr Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu	50	55 60
Pro Ala Ala Ile Phe Tyr Leu Pro Lys Arg His Arg Lys Val Cys	65	70 75
Gly Asn Pro Lys Ser Arg Glu Val Gln Arg Ala Met Lys Leu Leu	80	85 90
Asp Ala Arg Asn Lys Val Phe Ala Lys Leu Arg His Asn Thr Gln	95	100 105
Thr Phe Gln Ala Gly Pro His Ala Val Lys Lys Leu Ser Ser Gly	110	115 120
Asn Ser Lys Leu Ser Ser Ser Lys Phe Ser Asn Pro Ile Ser Ser	125	130 135
Ser Lys Arg Asn Val Ser Leu Leu Ile Ser Ala Asn Ser Gly Leu	140	145 150

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 217 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: UTRSN06
 - (B) CLONE: 1638407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26 :

Met Ala Pro Pro Ala Leu Gln Arg Gly Gln Arg Val Ala Ala Val	5	10 15
-------------------------------------------------------------	---	-------

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSTUT08
(B) CLONE: 1653112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27 :

Met	Ser	Gln	Pro	Arg	Thr	Pro	Glu	Gln	Ala	Leu	Asp	Thr	Pro	Gly	5	10	15
Asp	Cys	Pro	Pro	Gly	Arg	Arg	Asp	Glu	Asp	Ala	Gly	Glu	Gly	Ile	20	25	30
Gln	Cys	Ser	Gln	Arg	Met	Leu	Ser	Phe	Ser	Asp	Ala	Leu	Leu	Ser	35	40	45
Ile	Ile	Ala	Thr	Val	Met	Ile	Leu	Pro	Val	Thr	His	Thr	Glu	Ile	50	55	60
Ser	Pro	Glu	Gln	Gln	Phe	Asp	Arg	Ser	Val	Gln	Arg	Leu	Leu	Ala	65	70	75
Thr	Arg	Ile	Ala	Val	Tyr	Leu	Met	Thr	Phe	Leu	Ile	Val	Thr	Val	80	85	90
Ala	Trp	Ala	Ala	His	Thr	Arg	Leu	Phe	Gln	Val	Val	Gly	Lys	Thr	95	100	105
Asp	Asp	Thr	Leu	Ala	Leu	Leu	Asn	Leu	Ala	Cys	Met	Met	Thr	Ile			

	110		115		120									
Thr	Phe	Leu	Pro	Tyr	Thr	Phe	Ser	Leu	Met	Val	Thr	Phe	Pro	Asp
				125					130					135
Val	Pro	Leu	Gly	Ile	Phe	Leu	Phe	Cys	Val	Cys	Val	Ile	Ala	Ile
				140					145					150
Gly	Val	Val	Gln	Ala	Leu	Ile	Val	Gly	Tyr	Ala	Phe	His	Phe	Pro
				155					160					165
His	Leu	Leu	Ser	Pro	Gln	Ile	Gln	Arg	Ser	Ala	His	Arg	Ala	Leu
				170					175					180
Tyr	Arg	Arg	His	Val	Leu	Gly	Ile	Val	Leu	Gln	Gly	Pro	Ala	Leu
				185					190					195
Cys	Phe	Ala	Ala	Ala	Ile	Phe	Ser	Leu	Phe	Phe	Val	Pro	Leu	Ser
				200					205					210
Tyr	Leu	Leu	Met	Val	Thr	Val	Ile	Leu	Leu	Pro	Tyr	Val	Ser	Lys
				215					220					225
Val	Thr	Gly	Trp	Cys	Arg	Asp	Arg	Leu	Leu	Gly	His	Arg	Glu	Pro
				230					235					240
Ser	Ala	His	Pro	Val	Glu	Val	Phe	Ser	Phe	Asp	Leu	His	Glu	Pro
				245					250					255
Leu	Ser	Lys	Glu	Arg	Val	Glu	Ala	Phe	Ser	Asp	Gly	Val	Tyr	Ala
				260					265					270
Ile	Val	Ala	Thr	Leu	Leu	Ile	Leu	Asp	Ile	Cys	Glu	Asp	Asn	Val
				275					280					285
Pro	Asp	Pro	Lys	Asp	Val	Lys	Glu	Arg	Phe	Ser	Gly	Ser	Leu	Val
				290					295					300
Ala	Ala	Leu	Ser	Ala	Thr	Gly	Pro	Arg	Phe	Leu	Ala	Tyr	Phe	Gly
				305					310					315
Ser	Phe	Ala	Thr	Val	Gly	Leu	Leu	Trp	Phe	Ala	His	His	Ser	Leu
				320					325					330
Phe	Leu	His	Val	Arg	Lys	Ala	Thr	Arg	Ala	Met	Gly	Leu	Leu	Asn
				335					340					345
Thr	Leu	Ser	Leu	Ala	Phe	Val	Gly	Gly	Leu	Pro	Leu	Ala	Tyr	Gln
				350					355					360
Gln	Thr	Ser	Ala	Phe	Ala	Arg	Gln	Pro	Arg	Asp	Glu	Leu	Glu	Arg
				365					370					375
Val	Arg	Val	Ser	Cys	Thr	Ile	Ile	Phe	Leu	Ala	Ser	Ile	Phe	Gln
				380					385					390
Leu	Ala	Met	Trp	Thr	Thr	Ala	Leu	Leu	His	Gln	Ala	Glu	Thr	Leu
				395					400					405
Gln	Pro	Ser	Val	Trp	Phe	Gly	Gly	Arg	Glu	His	Val	Leu	Met	Phe
				410					415					420
Ala	Lys	Leu	Ala	Leu	Tyr	Pro	Cys	Ala	Ser	Leu	Leu	Ala	Phe	Ala
				425					430					435
Ser	Thr	Cys	Leu	Leu	Ser	Arg	Phe	Ser	Val	Gly	Ile	Phe	His	Leu
				440					445					450
Met	Gln	Ile	Ala	Val	Pro	Cys	Ala	Phe	Leu	Leu	Leu	Arg	Leu	Leu
				455					460					465
Val	Gly	Leu	Ala	Leu	Ala	Thr	Leu	Arg	Val	Leu	Arg	Gly	Leu	Ala
				470					475					480
Arg	Pro	Glu	His	Pro	Pro	Pro	Ala	Pro	Thr	Gly	Gln	Asp	Asp	Pro
				485					490					495
Gln	Ser	Gln	Leu	Leu	Pro	Ala	Pro	Cys						
				500										

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 320 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: BRSTNOT09
 (B) CLONE: 1664634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28 :

Met Ala Ala Arg Leu Asp Gly Gly Phe Ala Ala Val Ser Arg Ala
 5 10 15
 Phe His Glu Ile Arg Ala Arg Asn Pro Ala Phe Gln Pro Gln Thr
 20 25 30
 Leu Met Asp Phe Gly Ser Gly Thr Gly Ser Val Thr Trp Ala Ala
 35 40 45
 His Ser Ile Trp Gly Gln Ser Leu Arg Glu Tyr Met Cys Val Asp
 50 55 60
 Arg Ser Ala Ala Met Leu Val Leu Ala Glu Lys Leu Leu Thr Gly
 65 70 75
 Gly Ser Glu Ser Gly Glu Pro Tyr Ile Pro Gly Val Phe Phe Arg
 80 85 90
 Gln Phe Leu Pro Val Ser Pro Lys Val Gln Phe Asp Val Val Val
 95 100 105
 Ser Ala Phe Ser Leu Ser Asp Gln Leu Leu Thr Phe Ile Leu Ser
 110 115 120
 Cys Asn Ser Ser Leu Leu His Ile Phe Pro Phe Cys Glu Gln Val
 125 130 135
 Leu Val Glu Asn Gly Thr Lys Ala Gly His Ser Leu Leu Met Asp
 140 145 150
 Ala Arg Asp Leu Val Leu Lys Gly Lys Glu Lys Ser Pro Leu Asp
 155 160 165
 Pro Arg Pro Gly Phe Val Phe Ala Pro Cys Pro His Glu Leu Pro
 170 175 180
 Cys Pro Gln Leu Thr Asn Leu Ala Cys Ser Phe Ser Gln Ala Tyr
 185 190 195
 His Pro Ile Pro Phe Ser Trp Asn Lys Lys Pro Lys Glu Glu Lys
 200 205 210
 Phe Ser Met Val Ile Leu Ala Arg Gly Ser Pro Glu Glu Ala His
 215 220 225
 Arg Trp Pro Arg Ile Thr Gln Pro Val Leu Lys Arg Pro Arg His
 230 235 240
 Val His Cys His Leu Cys Cys Pro Asp Gly His Met Gln His Ala
 245 250 255
 Val Leu Thr Ala Arg Arg His Gly Arg Tyr Gly Gly Cys Asp Gln
 260 265 270
 Asn Gln Trp Asp Val Ala Gly Ser Cys Ser Pro Arg Gln His Leu
 275 280 285
 Phe Pro Gln Gly Phe Val Ser Leu Cys Pro Cys Gln Leu Leu Gly
 290 295 300
 Arg Ser Phe Thr Cys Ala Tyr Ser Val Cys Val Ser Ser Ile Tyr
 305 310 315
 Gly Ser Gly Ser Leu
 320

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: PROSTUT10
 - (B) CLONE: 1690990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29 :

Met	Asp	Asn	Lys	Gly	Ile	Tyr	Pro	Gly	Ala	Val	Phe	Tyr	His	Asp
				5					10					15
Ser	Phe	Thr	Glu	Ser	Arg	Val	Val	Leu	Leu	Arg	Ile	Arg	Thr	Leu
				20					25					30
Val	Pro	Tyr	Ser	Pro	Pro	Asp	Cys	Pro	Thr	Thr	Thr	Thr	Ala	Tyr
				35					40					45
Ser	Pro	Phe	Pro	Asn	His	Gly	Gln	Ile	Glu	Leu	Leu	Thr	Glu	
				50					55					60
Val	Ser	Phe	Arg	Trp	Ile	Ser	Gln	Pro	Phe	Pro	His	Arg	Pro	His
				65					70					75
Arg	Glu	Thr	Val	Thr	Asp	Cys	Tyr	Ser	Pro	Asn	Thr	Gln	Val	Lys
				80					85					90
Ser	Asn	Ala	Gly	Arg	Asn	Asn	Ser	Lys	Ser	Phe	Asn	Phe	Leu	Ile
				95					100					105
Leu	Leu	Leu	Lys	Ile	Leu	Thr	Glu	Ala	Ser	Arg	Phe			
				110					115					

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 298 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: DUODNOT02
 - (B) CLONE: 1704050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30 :

Met	Ala	Arg	Arg	Ser	Arg	His	Arg	Leu	Leu	Leu	Leu	Leu	Arg	
					5			10					15	
Tyr	Leu	Val	Val	Ala	Leu	Gly	Tyr	His	Lys	Ala	Tyr	Gly	Phe	Ser
					20				25					30
Ala	Pro	Lys	Asp	Gln	Gln	Val	Val	Thr	Ala	Val	Glu	Tyr	Gln	Glu
				35					40					45
Ala	Ile	Leu	Ala	Cys	Lys	Thr	Pro	Lys	Thr	Val	Ser	Ser	Arg	
				50					55					60
Leu	Glu	Trp	Lys	Lys	Leu	Gly	Arg	Ser	Val	Ser	Phe	Val	Tyr	Tyr
				65					70					75
Gln	Gln	Thr	Leu	Gln	Gly	Asp	Phe	Lys	Asn	Arg	Ala	Glu	Met	Ile
				80					85					90
Asp	Phe	Asn	Ile	Arg	Ile	Lys	Asn	Val	Thr	Arg	Ser	Asp	Ala	Gly
				95					100					105
Lys	Tyr	Arg	Cys	Glu	Val	Ser	Ala	Pro	Ser	Glu	Gln	Gly	Gln	Asn
				110					115					120

Leu	Glu	Glu	Asp	Thr	Val	Thr	Leu	Glu	Val	Leu	Val	Ala	Pro	Ala
					125				130					135
Val	Pro	Ser	Cys	Glu	Val	Pro	Ser	Ser	Ala	Leu	Ser	Gly	Thr	Val
					140				145					150
Val	Glu	Leu	Arg	Cys	Gln	Asp	Lys	Glu	Gly	Asn	Pro	Ala	Pro	Glu
					155				160					165
Tyr	Thr	Trp	Phe	Lys	Asp	Gly	Ile	Arg	Leu	Leu	Glu	Asn	Pro	Arg
					170				175					180
Leu	Gly	Ser	Gln	Ser	Thr	Asn	Ser	Ser	Tyr	Thr	Met	Asn	Thr	Lys
					185				190					195
Thr	Gly	Thr	Leu	Gln	Phe	Asn	Thr	Val	Ser	Lys	Leu	Asp	Thr	Gly
					200				205					210
Glu	Tyr	Ser	Cys	Glu	Ala	Arg	Asn	Ser	Val	Gly	Tyr	Arg	Arg	Cys
					215				220					225
Pro	Gly	Lys	Arg	Met	Gln	Val	Asp	Asp	Leu	Asn	Ile	Ser	Gly	Ile
					230				235					240
Ile	Ala	Ala	Val	Val	Val	Val	Ala	Leu	Val	Ile	Ser	Val	Cys	Gly
					245				250					255
Leu	Gly	Val	Cys	Tyr	Ala	Gln	Arg	Lys	Gly	Tyr	Phe	Ser	Lys	Glu
					260				265					270
Thr	Ser	Phe	Gln	Lys	Ser	Asn	Ser	Ser	Ser	Lys	Ala	Thr	Thr	Met
					275				280					285
Ser	Glu	Asn	Asp	Phe	Lys	His	Thr	Lys	Ser	Phe	Ile	Ile		
					290				295					

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSN0T16
- (B) CLONE: 1711840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31 :

Met	Gln	His	Arg	Gly	Phe	Leu	Leu	Leu	Thr	Leu	Leu	Ala	Leu	Leu
					5				10					15
Ala	Leu	Thr	Ser	Ala	Val	Ala	Lys	Lys	Gln	Asp	Lys	Val	Lys	Lys
					20				25					30
Gly	Gly	Pro	Gly	Ser	Glu	Cys	Ala	Glu	Trp	Ala	Trp	Gly	Pro	Cys
					35				40					45
Thr	Pro	Ser	Ser	Lys	Gly	Phe	Ala	Ala	Val	Gly	Phe	Pro	Arg	Gly
					50				55					60
Pro	Pro	Trp	Gly	Gly	Pro	Arg	Thr	Gln	Pro	Ala	Val	Leu	Val	Glu
					65				70					75
Arg	Val	Ala	Pro	Gly	Lys	Leu	Glu	Arg	Lys	Glu	Phe	Trp	Ala	Pro
					80				85					90
Gly	Leu	Trp	Lys	Val	Gly	Gln	Ile	Phe	Trp	Lys	Lys	Thr	Trp	Arg
					95				100					105
Val	Cys	Arg	Ser	Val	Lys	Trp	Gly	Arg	Gly	Gln	Lys	Asn		
					110				115					

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32 :

Met	Gln	Thr	Cys	Pro	Leu	Ala	Phe	Pro	Gly	His	Val	Ser	Gln	Ala	
5									10					15	
Leu	Gly	Thr	Leu	Leu	Phe	Leu	Ala	Ala	Ser	Leu	Ser	Ala	Gln	Asn	
	20								25					30	
Glu	Gly	Trp	Asp	Ser	Pro	Ile	Cys	Thr	Glu	Gly	Val	Val	Ser	Val	
	35								40					45	
Ser	Trp	Gly	Glu	Asn	Thr	Val	Met	Ser	Cys	Asn	Ile	Ser	Asn	Ala	
	50								55					60	
Phe	Ser	His	Val	Asn	Ile	Lys	Leu	Arg	Ala	His	Gly	Gln	Glu	Ser	
	65								70					75	
Ala	Ile	Phe	Asn	Glu	Val	Ala	Pro	Gly	Tyr	Phe	Ser	Arg	Asp	Gly	
	80								85					90	
Trp	Gln	Leu	Gln	Val	Gln	Gly	Gly	Val	Ala	Gln	Leu	Val	Ile	Lys	
	95								100					105	
Gly	Ala	Arg	Asp	Ser	His	Ala	Gly	Leu	Tyr	Met	Trp	His	Leu	Val	
	110								115					120	
Gly	His	Gln	Arg	Asn	Asn	Arg	Gln	Val	Thr	Leu	Glu	Val	Ser	Gly	
	125								130					135	
Ala	Glu	Pro	Gln	Ser	Ala	Pro	Asp	Thr	Gly	Phe	Trp	Pro	Val	Pro	
	140								145					150	
Ala	Val	Val	Thr	Ala	Val	Phe	Ile	Leu	Leu	Val	Ala	Leu	Val	Met	
	155								160					165	
Phe	Ala	Trp	Tyr	Arg	Cys	Arg	Cys	Ser	Gln	Gln	Arg	Arg	Glu	Lys	
	170								175					180	
Lys	Phe	Phe	Leu	Leu	Glu	Pro	Gln	Met	Lys	Val	Ala	Ala	Leu	Arg	
	185								190					195	
Ala	Gly	Ala	Gln	Gln	Gly	Leu	Ser	Arg	Ala	Ser	Ala	Glu	Leu	Trp	
	200								205					210	
Thr	Pro	Asp	Ser	Glu	Pro	Thr	Pro	Arg	Pro	Leu	Ala	Leu	Val	Phe	
	215								220					225	
Lys	Pro	Ser	Pro	Leu	Gly	Ala	Leu	Glu	Leu	Leu	Ser	Pro	Gln	Pro	
	230								235					240	
Leu	Phe	Pro	Tyr	Ala	Ala	Asp	Pro								
	245														

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: STOMTUT02
 (B) CLONE: 1750632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33 :

Met	Leu	Glu	Glu	Gly	Ser	Phe	Arg	Gly	Arg	Thr	Ala	Asp	Phe	Val
5							10						15	
Phe	Met	Phe	Leu	Phe	Gly	Gly	Val	Leu	Met	Thr	Val	Ser	Phe	Pro
	20						25						30	
Gln	Ala	Leu	Glu	Pro	Arg	Ala	Arg	Ala	Pro	Arg	Arg	Pro	Ala	Cys
	35						40						45	
Val	Gly	Pro	Gly	Ala	Asn	Thr	Ala	Met	Pro	Glu	Arg	Asp	Thr	Val
	50						55						60	
Ala	Val	Ser	Ser	Leu	Ala	Pro	Phe	Leu	Pro	Trp	Ala	Leu	Met	Gly
	65						70						75	
Phe	Ser	Leu	Leu	Leu	Gly	Asn	Ser	Ile	Leu	Val	Asp	Leu	Leu	Gly
	80						85						90	
Ile	Ala	Val	Gly	His	Ile	Tyr	Tyr	Phe	Leu	Glu	Asp	Val	Phe	Pro
	95						100						105	
Asn	Gln	Pro	Gly	Gly	Lys	Arg	Leu	Leu	Gln	Thr	Pro	Gly	Phe	Leu
	110						115						120	
Lys	Leu	Leu	Leu	Asp	Ala	Pro	Ala	Glu	Asp	Pro	Asn	Tyr	Leu	Pro
	125						130						135	
Leu	Pro	Glu	Glu	Gln	Pro	Gly	Pro	His	Leu	Pro	Pro	Pro	Gln	Gln
	140						145						150	

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 431 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34 :

Met	Trp	Ala	Leu	Gly	Gln	Ala	Gly	Phe	Ala	Asn	Leu	Thr	Glu	Gly
5								10					15	
Leu	Lys	Val	Trp	Leu	Gly	Ile	Met	Leu	Pro	Val	Leu	Gly	Ile	Lys
	20							25					30	
Ser	Leu	Ser	Pro	Phe	Ala	Ile	Thr	Tyr	Leu	Asp	Arg	Leu	Leu	Leu
	35							40					45	
Met	His	Pro	Asn	Leu	Thr	Lys	Gly	Phe	Gly	Met	Ile	Gly	Pro	Lys
	50							55					60	
Asp	Phe	Phe	Pro	Leu	Leu	Asp	Phe	Ala	Tyr	Met	Pro	Asn	Asn	Ser
	65							70					75	
Leu	Thr	Pro	Ser	Leu	Gln	Glu	Gln	Leu	Cys	Gln	Leu	Tyr	Pro	Arg
	80							85					90	
Leu	Lys	Met	Leu	Ala	Phe	Gly	Ala	Lys	Pro	Asp	Ser	Thr	Leu	His
	95							100					105	
Thr	Tyr	Phe	Pro	Ser	Phe	Leu	Ser	Arg	Ala	Thr	Pro	Ser	Cys	Pro
	110							115					120	

Pro	Glu	Met	Lys	Lys	Glu	Leu	Leu	Ser	Ser	Leu	Thr	Glu	Cys	Leu
					125					130				135
Thr	Val	Asp	Pro	Leu	Ser	Ala	Ser	Val	Trp	Arg	Gln	Leu	Tyr	Pro
				140					145					150
Lys	His	Leu	Ser	Gln	Ser	Ser	Leu	Leu	Leu	Glu	His	Leu	Leu	Ser
				155					160					165
Ser	Trp	Glu	Gln	Ile	Pro	Lys	Lys	Val	Gln	Lys	Ser	Leu	Gln	Glu
				170					175					180
Thr	Ile	Gln	Ser	Leu	Lys	Leu	Thr	Asn	Gln	Glu	Leu	Leu	Arg	Lys
				185					190					195
Gly	Ser	Ser	Asn	Asn	Gln	Asp	Val	Val	Thr	Cys	Asp	Met	Ala	Cys
				200					205					210
Lys	Gly	Leu	Leu	Gln	Gln	Val	Gln	Gly	Pro	Arg	Leu	Pro	Trp	Thr
				215					220					225
Arg	Leu	Leu	Leu	Leu	Leu	Leu	Val	Phe	Ala	Val	Gly	Phe	Leu	Cys
					230				235					240
His	Asp	Leu	Arg	Ser	His	Ser	Ser	Phe	Gln	Ala	Ser	Leu	Thr	Gly
				245					250					255
Arg	Leu	Leu	Arg	Ser	Ser	Gly	Phe	Leu	Pro	Ala	Ser	Gln	Gln	Ala
				260					265					270
Cys	Ala	Lys	Leu	Tyr	Ser	Tyr	Ser	Leu	Gln	Gly	Tyr	Ser	Trp	Leu
				275					280					285
Gly	Glu	Thr	Leu	Pro	Leu	Trp	Gly	Ser	His	Leu	Leu	Thr	Val	Val
				290					295					300
Arg	Pro	Ser	Leu	Gln	Leu	Ala	Trp	Ala	His	Thr	Asn	Ala	Thr	Val
				305					310					315
Ser	Phe	Leu	Ser	Ala	His	Cys	Ala	Ser	His	Leu	Ala	Trp	Phe	Gly
				320					325					330
Asp	Ser	Leu	Thr	Ser	Leu	Ser	Gln	Arg	Leu	Gln	Ile	Gln	Leu	Pro
				335					340					345
Asp	Ser	Val	Asn	Gln	Leu	Leu	Arg	Tyr	Leu	Arg	Glu	Leu	Pro	Leu
				350					355					360
Leu	Phe	His	Gln	Asn	Val	Leu	Leu	Pro	Leu	Trp	His	Leu	Leu	Leu
				365					370					375
Glu	Ala	Leu	Ala	Trp	Ala	Gln	Glu	His	Cys	His	Glu	Ala	Cys	Arg
				380					385					390
Gly	Glu	Val	Thr	Trp	Asp	Cys	Met	Lys	Thr	Gln	Leu	Ser	Glu	Ala
				395					400					405
Val	His	Trp	Thr	Trp	Leu	Cys	Leu	Gln	Asp	Ile	Thr	Val	Ala	Phe
				410					415					420
Leu	Asp	Trp	Ala	Leu	Ala	Leu	Ile	Ser	Gln	Gln				
				425					430					

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 278 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: PROSN0T20
 - (B) CLONE: 1818761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35 :

Met	Gln	Trp	Leu	Arg	Val	Arg	Glu	Ser	Pro	Gly	Glu	Ala	Thr	Gly
										5	10			15
His	Arg	Val	Thr	Met	Gly	Thr	Ala	Ala	Leu	Gly	Pro	Val	Trp	Ala
										20	25			30
Ala	Leu	Leu	Leu	Phe	Leu	Leu	Met	Cys	Glu	Ile	Pro	Met	Val	Glu
										35	40			45
Leu	Thr	Phe	Asp	Arg	Ala	Val	Ala	Ser	Gly	Cys	Gln	Arg	Cys	Cys
										50	55			60
Asp	Ser	Glu	Asp	Pro	Leu	Asp	Pro	Ala	His	Val	Ser	Ser	Ala	Ser
										65	70			75
Ser	Ser	Gly	Arg	Pro	His	Ala	Leu	Pro	Glu	Ile	Arg	Pro	Tyr	Ile
										80	85			90
Asn	Ile	Thr	Ile	Leu	Lys	Gly	Asp	Lys	Gly	Asp	Pro	Gly	Pro	Met
										95	100			105
Gly	Leu	Pro	Gly	Tyr	Met	Gly	Arg	Glu	Gly	Pro	Gln	Gly	Glu	Pro
										110	115			120
Gly	Pro	Gln	Gly	Ser	Lys	Gly	Asp	Lys	Gly	Glu	Met	Gly	Ser	Pro
										125	130			135
Gly	Ala	Pro	Cys	Gln	Lys	Arg	Phe	Phe	Ala	Phe	Ser	Val	Gly	Arg
										140	145			150
Lys	Thr	Ala	Leu	His	Ser	Gly	Glu	Asp	Phe	Gln	Thr	Leu	Leu	Phe
										155	160			165
Glu	Arg	Val	Phe	Val	Asn	Leu	Asp	Gly	Cys	Phe	Asp	Met	Ala	Thr
										170	175			180
Gly	Gln	Phe	Ala	Ala	Pro	Leu	Arg	Gly	Ile	Tyr	Phe	Phe	Ser	Leu
										185	190			195
Asn	Val	His	Ser	Trp	Asn	Tyr	Lys	Glu	Thr	Tyr	Val	His	Ile	Met
										200	205			210
His	Asn	Gln	Lys	Glu	Ala	Val	Ile	Leu	Tyr	Ala	Gln	Pro	Ser	Glu
										215	220			225
Arg	Ser	Ile	Met	Gln	Ser	Gln	Ser	Val	Met	Leu	Asp	Leu	Ala	Tyr
										230	235			240
Gly	Asp	Arg	Val	Trp	Val	Arg	Leu	Phe	Lys	Arg	Gln	Arg	Glu	Asn
										245	250			255
Ala	Ile	Tyr	Ser	Asn	Asp	Phe	Asp	Thr	Tyr	Ile	Thr	Phe	Ser	Gly
										260	265			270
His	Leu	Ile	Lys	Ala	Glu	Asp	Asp							
										275				

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GBLATUT01
- (B) CLONE: 1824469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36 :

Met	Glu	Glu	Lys	Arg	Arg	Ala	Arg	Val	Gln	Gly	Ala	Trp	Ala	
									5	10			15	
Ala	Pro	Val	Lys	Ser	Gln	Ala	Ile	Ala	Gln	Pro	Ala	Thr	Thr	Ala

20	25	30
Lys Ser His Leu His Gln Lys Pro Gly Gln	Thr Trp Lys Asn Lys	
35	40	45
Glu His His Leu Ser Asp Arg Glu Phe Val	Phe Lys Glu Pro Gln	
50	55	60
Gln Val Val Arg Arg Ala Pro Glu Pro Arg	Val Ile Asp Arg Glu	
65	70	75
Gly Val Tyr Glu Ile Ser Leu Ser Pro Thr	Gly Val Ser Arg Val	
80	85	90
Cys Leu Tyr Pro Gly Phe Val Asp Val	Lys Glu Ala Asp Trp Ile	
95	100	105
Leu Glu Gln Leu Cys Gln Asp Val Pro	Trp Lys Gln Arg Thr Gly	
110	115	120
Ile Arg Glu Asp Ile Thr Tyr Gln Gln	Pro Arg Leu Thr Ala Trp	
125	130	135
Tyr Gly Glu Leu Pro Tyr Thr Tyr Ser Arg	Ile Thr Met Glu Pro	
140	145	150
Asn Pro His Trp His Pro Val Leu Arg Thr	Leu Lys Asn Arg Ile	
155	160	165
Glu Glu Asn Thr Gly His Thr Phe Asn Ser	Leu Leu Cys Asn Leu	
170	175	180
Tyr Arg Asn Glu Lys Asp Ser Val Asp	Trp His Ser Asp Asp Glu	
185	190	195
Pro Ser Leu Gly Arg Cys Pro Ile Ile	Ala Ser Leu Ser Phe Gly	
200	205	210
Ala Thr Arg Thr Phe Glu Met Arg Lys	Lys Pro Pro Pro Glu Glu	
215	220	225
Asn Gly Asp Tyr Thr Tyr Val Glu Arg Val	Lys Ile Pro Leu Asp	
230	235	240
His Gly Thr Leu Leu Ile Met Glu Gly	Ala Thr Gln Ala Asp Trp	
245	250	255
Gln His Arg Val Pro Lys Glu Tyr His	Ser Arg Glu Pro Arg Val	
260	265	270
Asn Leu Thr Phe Arg Thr Val Tyr Pro	Asp Pro Arg Gly Ala Pro	
275	280	285
Trp		

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 404 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: PROSNOT19
 - (B) CLONE: 1864292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37 :

Met Lys Met Glu Glu Ala Val Gly Lys Val Glu Glu Leu Ile Glu		
5	10	15
Ser Glu Ala Pro Pro Lys Ala Ser Glu Gln Glu Thr Ala Lys Glu		
20	25	30
Glu Asp Gly Ser Val Glu Leu Glu Ser Gln Val Gln Lys Asp Gly		
35	40	45

Val	Ala	Asp	Ser	Thr	Val	Ile	Ser	Ser	Met	Pro	Cys	Leu	Leu	Met
					50				55					60
Glu	Leu	Arg	Arg	Asp	Ser	Ser	Glu	Ser	Gln	Leu	Ala	Ser	Thr	Glu
					65				70					75
Ser	Asp	Lys	Pro	Thr	Thr	Gly	Arg	Val	Tyr	Glu	Ser	Asp	Pro	Ser
					80				85					90
Asn	His	Cys	Met	Leu	Ser	Pro	Ser	Ser	Gly	His	Leu	Ala	Asp	
					95				100					105
Ser	Asp	Thr	Leu	Ser	Ser	Ala	Glu	Glu	Asn	Glu	Pro	Ser	Gln	Ala
					110				115					120
Glu	Thr	Ala	Val	Glu	Gly	Asp	Pro	Ser	Gly	Val	Ser	Gly	Ala	Thr
					125				130					135
Val	Gly	Arg	Lys	Ser	Arg	Arg	Ser	Arg	Ser	Glu	Ser	Glu	Thr	Ser
					140				145					150
Thr	Met	Ala	Ala	Lys	Lys	Asn	Arg	Gln	Ser	Ser	Asp	Lys	Gln	Asn
					155				160					165
Gly	Arg	Val	Ala	Lys	Val	Lys	Gly	His	Arg	Ser	Gln	Lys	His	Lys
					170				175					180
Glu	Arg	Ile	Arg	Leu	Leu	Arg	Gln	Lys	Arg	Glu	Ala	Ala	Ala	Arg
					185				190					195
Lys	Lys	Tyr	Asn	Leu	Leu	Gln	Asp	Ser	Ser	Thr	Ser	Asp	Ser	Asp
					200				205					210
Leu	Thr	Cys	Asp	Ser	Ser	Thr	Ser	Ser	Ser	Asp	Asp	Asp	Glu	Glu
					215				220					225
Val	Ser	Gly	Ser	Ser	Lys	Thr	Ile	Thr	Ala	Glu	Ile	Pro	Asp	Gly
					230				235					240
Pro	Pro	Val	Val	Ala	His	Tyr	Asp	Met	Ser	Asp	Thr	Asn	Ser	Asp
					245				250					255
Pro	Glu	Val	Val	Asn	Val	Asp	Asn	Leu	Leu	Ala	Ala	Ala	Val	Val
					260				265					270
Gln	Glu	His	Ser	Asn	Ser	Val	Gly	Gly	Gln	Asp	Thr	Gly	Ala	Thr
					275				280					285
Trp	Arg	Thr	Ser	Gly	Leu	Leu	Glu	Glu	Leu	Asn	Ala	Glu	Ala	Gly
					290				295					300
His	Leu	Asp	Pro	Gly	Phe	Leu	Ala	Ser	Asp	Lys	Thr	Ser	Ala	Gly
					305				310					315
Asn	Ala	Pro	Leu	Asn	Glu	Glu	Ile	Asn	Ile	Ala	Ser	Ser	Asp	Ser
					320				325					330
Glu	Val	Glu	Ile	Val	Gly	Val	Gln	Glu	His	Ala	Arg	Cys	Val	His
					335				340					345
Pro	Arg	Gly	Gly	Val	Ile	Gln	Ser	Val	Ser	Ser	Trp	Lys	His	Gly
					350				355					360
Ser	Gly	Thr	Gln	Tyr	Val	Ser	Thr	Arg	Gln	Thr	Gln	Ser	Trp	Thr
					365				370					375
Ala	Val	Thr	Pro	Gln	Gln	Thr	Trp	Ala	Ser	Pro	Ala	Glu	Val	Val
					380				385					390
Asp	Leu	Thr	Leu	Asp	Glu	Asp	Ser	Arg	Arg	Lys	Tyr	Leu	Leu	
					395				400					

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 405 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:

(A) LIBRARY: THP1NOT01
(B) CLONE: 1866437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38 :

Met Phe Val Gln Glu Glu Lys Ile Phe Ala Gly Lys Val Leu Arg
5 10 15
Leu His Ile Cys Ala Ser Asp Gly Ala Glu Trp Leu Glu Glu Ala
20 25 30
Thr Glu Asp Thr Ser Val Glu Lys Leu Lys Glu Arg Cys Leu Lys
35 40 45
His Cys Ala His Gly Ser Leu Glu Asp Pro Lys Ser Ile Thr His
50 55 60
His Lys Leu Ile His Ala Ala Ser Glu Arg Val Leu Ser Asp Ala
65 70 75
Arg Thr Ile Leu Glu Glu Asn Ile Gln Asp Gln Asp Val Leu Leu
80 85 90
Leu Lys Lys Lys Arg Ala Pro Ser Pro Leu Pro Lys Met Ala Asp
95 100 105
Val Ser Ala Glu Glu Lys Lys Lys Gln Asp Gln Lys Ala Pro Asp
110 115 120
Lys Glu Ala Ile Leu Arg Ala Thr Ala Asn Leu Pro Ser Tyr Asn
125 130 135
Met Asp Arg Ala Ala Val Gln Thr Asn Met Arg Asp Phe Gln Thr
140 145 150
Glu Leu Arg Lys Ile Leu Val Ser Leu Ile Glu Val Ala Gln Lys
155 160 165
Leu Leu Ala Leu Asn Pro Asp Ala Val Glu Leu Phe Lys Lys Ala
170 175 180
Asn Ala Met Leu Asp Glu Asp Glu Asp Glu Arg Val Asp Glu Ala
185 190 195
Ala Leu Arg Gln Leu Thr Glu Met Gly Phe Pro Glu Asn Arg Ala
200 205 210
Thr Lys Ala Leu Gln Leu Asn His Met Ser Val Pro Gln Ala Met
215 220 225
Glu Trp Leu Ile Glu His Ala Glu Asp Pro Thr Ile Asp Thr Pro
230 235 240
Leu Pro Gly Gln Ala Pro Pro Glu Ala Glu Gly Ala Thr Ala Ala
245 250 255
Ala Ser Glu Ala Ala Ala Gly Ala Ser Ala Thr Asp Glu Glu Ala
260 265 270
Arg Asp Glu Leu Thr Glu Ile Phe Lys Ile Arg Arg Lys Arg
275 280 285
Glu Phe Arg Ala Asp Ala Arg Ala Val Ile Ser Leu Met Glu Met
290 295 300
Gly Phe Asp Glu Lys Glu Val Ile Asp Ala Leu Arg Val Asn Asn
305 310 315
Asn Gln Gln Asn Ala Ala Cys Glu Trp Leu Leu Gly Asp Arg Lys
320 325 330
Pro Ser Pro Glu Glu Leu Asp Lys Gly Ile Asp Pro Asp Ser Pro
335 340 345
Leu Phe Gln Ala Ile Leu Asp Asn Pro Val Val Gln Leu Gly Leu
350 355 360
Thr Asn Pro Lys Thr Leu Leu Ala Phe Glu Asp Met Leu Glu Asn
365 370 375
Pro Leu Asn Ser Thr Gln Trp Met Asn Asp Pro Glu Thr Gly Pro
380 385 390
Val Met Leu Gln Ile Ser Arg Ile Phe Gln Thr Leu Asn Arg Thr
395 400 405

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 177 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: SKINBIT01
 - (B) CLONE: 1871375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39 :

Met	Val	Met	His	Asn	Ser	Asp	Pro	Asn	Leu	His	Leu	Leu	Ala	Glu	
										5	10				15
Gly	Ala	Pro	Ile	Asp	Trp	Gly	Glu	Glu	Tyr	Ser	Asn	Ser	Gly	Gly	
										20	25				30
Gly	Gly	Ser	Pro	Ala	Pro	Ala	Pro	Arg	Ser	Gln	Pro	Pro	Ser	Arg	
										35	40				45
Lys	Ser	Asp	Gly	Ala	Pro	Ser	Arg	Trp	Ser	Leu	Trp	Ser	Arg	Met	
										50	55				60
Arg	Arg	Trp	Gly	Cys	Pro	Leu	Arg	Leu	Ala	Leu	Ser	His	His	His	
										65	70				75
Leu	Arg	Pro	Arg	Thr	Val	Ser	Leu	Arg	Ser	Glu	Ala	Cys	Trp	Pro	
										80	85				90
Lys	Val	Cys	Gly	Leu	Arg	Ala	Pro	His	Gln	Pro	Ala	Pro	Cys	Ser	
										95	100				105
Thr	Gly	Pro	Pro	Leu	Gly	Arg	Val	Pro	Ser	Leu	Arg	Pro	Pro	Pro	
										110	115				120
Arg	Pro	Pro	Arg	Arg	Leu	Pro	His	Pro	Ser	Ser	Ile	Ser	Cys	Leu	
										125	130				135
Glu	Arg	Leu	Trp	Thr	Leu	Gly	Pro	Pro	Ser	Pro	Ala	Thr	Arg	Arg	
										140	145				150
Leu	Glu	Ser	Arg	Cys	Pro	Ala	Pro	Ala	Ala	Thr	Pro	Pro	Ser	Thr	
										155	160				165
Pro	Pro	Pro	Arg	Xaa	Xaa	Phe	Lys	Gly	Cys	Lys	Lys	Asn			
										170	175				

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 197 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: LEUKNOT03
 - (B) CLONE: 1880830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40 :

Met	Ile	Thr	Cys	Arg	Val	Cys	Gln	Ser	Leu	Ile	Asn	Val	Glu	Gly	
										5	10				15
Lys	Met	His	Gln	His	Val	Val	Lys	Cys	Gly	Val	Cys	Asn	Glu	Ala	
										20	25				30

Thr Pro Ile Lys Asn Ala Pro Pro Gly Lys Lys Tyr Val Arg Cys
 35 40 45
 Pro Cys Asn Cys Leu Leu Ile Cys Lys Val Thr Ser Gln Arg Ile
 50 55 60
 Ala Cys Pro Arg Pro Tyr Cys Lys Arg Ile Ile Asn Leu Gly Pro
 65 70 75
 Val His Pro Gly Pro Leu Ser Pro Glu Pro Gln Pro Met Gly Val
 80 85 90
 Arg Val Ile Cys Gly His Cys Lys Asn Thr Phe Leu Trp Thr Glu
 95 100 105
 Phe Thr Asp Arg Thr Leu Ala Arg Cys Pro His Cys Arg Lys Val
 110 115 120
 Ser Ser Ile Gly Arg Arg Tyr Pro Arg Lys Arg Cys Ile Cys Cys
 125 130 135
 Phe Leu Leu Gly Leu Leu Ala Val Thr Ala Thr Gly Leu Ala
 140 145 150
 Phe Gly Thr Trp Lys His Ala Arg Arg Tyr Gly Gly Ile Tyr Ala
 155 160 165
 Ala Trp Ala Phe Val Ile Leu Leu Ala Val Leu Cys Leu Gly Arg
 170 175 180
 Ala Leu Tyr Trp Ala Cys Met Lys Val Ser His Pro Val Gln Asn
 185 190 195
 Phe Ser

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARNOT07
- (B) CLONE: 1905325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41 :

Met Leu Lys Asp Ile Ile Lys Glu Tyr Thr Asp Val Tyr Pro Glu
 5 10 15
 Ile Ile Glu Arg Ala Gly Tyr Ser Leu Glu Lys Val Phe Gly Ile
 20 25 30
 Gln Leu Lys Glu Ile Asp Lys Asn Asp His Leu Tyr Ile Leu Leu
 35 40 45
 Ser Thr Leu Glu Pro Thr Asp Ala Gly Ile Leu Gly Thr Thr Lys
 50 55 60
 Asp Ser Pro Lys Leu Gly Leu Leu Met Val Leu Leu Ser Ile Ile
 65 70 75
 Phe Met Asn Gly Asn Arg Ser Ser Glu Ala Val Ile Trp Glu Val
 80 85 90
 Leu Arg Lys Leu Gly Leu Arg Pro Gly Ile His His Ser Leu Phe
 95 100 105
 Gly Asp Val Lys Lys Leu Ile Thr Asp Glu Phe Val Lys Gln Lys
 110 115 120
 Tyr Leu Asp Tyr Ala Arg Val Pro Asn Ser Asn Pro Pro Glu Tyr
 125 130 135
 Glu Phe Phe Trp Gly Leu Arg Ser Tyr Tyr Glu Thr Ser Lys Met
 140 145 150
 Lys Val Leu Lys Phe Ala Cys Lys Val Gln Lys Lys Asp Pro Lys

	155		160		165									
Glu	Trp	Ala	Ala	Gln	Tyr	Arg	Glu	Ala	Met	Glu	Ala	Asp	Leu	Lys
				170			175		175					180
Ala	Ala	Ala	Glu	Ala	Ala	Ala	Glu	Ala	Lys	Ala	Arg	Ala	Glu	Ile
				185			190		190					195
Arg	Ala	Arg	Met	Gly	Ile	Gly	Leu	Gly	Ser	Glu	Asn	Ala	Ala	Gly
			200				205		205					210
Pro	Cys	Asn	Trp	Asp	Glu	Ala	Asp	Ile	Gly	Pro	Trp	Ala	Lys	Ala
			215				220		220					225
Arg	Ile	Gln	Ala	Gly	Ala	Glu	Ala	Lys	Ala	Lys	Ala	Gln	Glu	Ser
			230				235		235					240
Gly	Ser	Ala	Ser	Thr	Gly	Ala	Ser	Thr	Ser	Thr	Asn	Asn	Ser	Ala
			245				250		250					255
Ser	Ala	Ser	Ala	Ser	Thr	Ser	Gly	Gly	Phe	Ser	Ala	Gly	Ala	Ser
			260				265		265					270
Leu	Thr	Ala	Thr	Leu	Thr	Phe	Gly	Leu	Phe	Ala	Gly	Leu	Gly	Gly
			275				280		280					285
Ala	Gly	Ala	Ser	Thr	Ser	Gly	Ser	Ser	Gly	Ala	Cys	Gly	Phe	Ser
			290				295		295					300
Tyr	Lys													

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT01
- (B) CLONE: 1919931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42 :

Met	Arg	Thr	Leu	Glu	Asn	Gln	Gly	Phe	Lys	Ile	Leu	Pro	Phe	Leu
								5	10					15
Gly	Val	Lys	Glu	Val	Trp	Gln	Lys	Gln	Asn	Lys	Leu	Ile	Ser	Arg
								20	25					30
Phe	Ile	Thr	Cys	Gln	Phe	Phe	Leu	Tyr	Asn	Phe	Leu	Asp	Ser	Gly
								35	40					45
Ser	Ile	Trp	Val	Gln	Ala	Asp	Phe	Pro	Pro	Ile	Leu	Gln	Cys	Gly
								50	55					60
Cys	Phe	Leu	Phe	His	Pro	Trp	Thr	Leu	Gln	Glu	Ile	Ala	Pro	Cys
								65	70					75
Phe	Cys	Leu	Cys	Ile	Thr	Glu	Lys	Gly	Ser	Met	Lys	Val	Ala	Gln
								80	85					90
Val	Arg	Pro	Phe	His	Cys	Pro	Pro	Gly	Ala	Gly	Phe	Ala	Leu	Pro
								95	100					105
Ile	Leu	Gly	Leu	Leu	Gln	Gly	Leu	Val	Ile	Leu	His	Ser	Pro	Leu
								110	115					120
His	Ile	Ser	Gln	Val	Ser	Ala	Gln	Lys	Ser	Pro	Phe	Gly	Gly	Val
								125	130					135
Ser	Thr	Cys	His	Cys	Val	Cys	Lys	Ser	Ser	Phe	Ser	Phe	Phe	Leu
								140	145					150
Ala	His	Leu	Thr	Leu	Val	Met	Ser	Leu	Ile	Thr	Thr	Thr	Ile	
								155	160					

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 235 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: BRSTNOT04
 - (B) CLONE: 1969426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43 :

Met	Ser	Pro	Thr	Leu	Ser	Ser	Ile	Thr	Gln	Gly	Val	Pro	Leu	Asp	
									5	10					15
Thr	Ser	Lys	Leu	Ser	Thr	Asp	Gln	Arg	Leu	Pro	Pro	Tyr	Pro	Tyr	
									20	25					30
Ser	Ser	Pro	Ser	Leu	Val	Leu	Pro	Thr	Gln	Pro	His	Thr	Pro	Lys	
									35	40					45
Ser	Leu	Gln	Gln	Pro	Gly	Leu	Pro	Ser	Gln	Ser	Cys	Ser	Val	Gln	
									50	55					60
Ser	Ser	Gly	Gly	Gln	Pro	Pro	Gly	Arg	Gln	Ser	His	Tyr	Gly	Thr	
									65	70					75
Pro	Tyr	Pro	Pro	Gly	Pro	Ser	Gly	His	Gly	Gln	Gln	Ser	Tyr	His	
									80	85					90
Arg	Pro	Met	Ser	Asp	Phe	Asn	Leu	Gly	Asn	Leu	Glu	Gln	Phe	Ser	
									95	100					105
Met	Glu	Ser	Pro	Ser	Ala	Ser	Leu	Val	Leu	Asp	Pro	Pro	Gly	Phe	
									110	115					120
Ser	Glu	Gly	Pro	Gly	Phe	Leu	Gly	Gly	Glu	Gly	Pro	Met	Gly	Gly	
									125	130					135
Pro	Gln	Asp	Pro	His	Thr	Phe	Asn	His	Gln	Asn	Leu	Thr	His	Cys	
									140	145					150
Ser	Arg	His	Gly	Ser	Gly	Pro	Asn	Ile	Ile	Leu	Thr	Gly	Asp	Ser	
									155	160					165
Ser	Pro	Gly	Phe	Ser	Lys	Glu	Ile	Ala	Ala	Ala	Leu	Ala	Gly	Val	
									170	175					180
Pro	Gly	Phe	Glu	Val	Ser	Ala	Ala	Gly	Leu	Glu	Leu	Gly	Leu	Gly	
									185	190					195
Leu	Glu	Asp	Glu	Leu	Arg	Met	Glu	Pro	Leu	Gly	Leu	Glu	Gly	Leu	
									200	205					210
Asn	Met	Leu	Ser	Asp	Pro	Cys	Ala	Leu	Leu	Pro	Asp	Pro	Ala	Val	
									215	220					225
Glu	Glu	Ser	Phe	Arg	Ser	Asp	Arg	Leu	Gln						
									230	235					

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 203 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: UCMCL5T01

(B) CLONE: 1969948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44 :

Met	Asn	Tyr	Phe	Pro	Leu	Ala	Pro	Phe	Asn	Gln	Leu	Leu	Gln	Lys
5									10					15
Asp	Ile	Ile	Ser	Glu	Leu	Leu	Thr	Ser	Asp	Asp	Met	Lys	Asn	Ala
	20								25					30
Tyr	Lys	Leu	His	Thr	Leu	Asp	Thr	Cys	Leu	Lys	Leu	Asp	Asp	Thr
	35								40					45
Val	Tyr	Leu	Arg	Asp	Ile	Ala	Leu	Ser	Leu	Pro	Gln	Leu	Pro	Arg
	50								55					60
Glu	Leu	Pro	Ser	Ser	His	Thr	Asn	Ala	Lys	Val	Ala	Glu	Val	Leu
	65								70					75
Ser	Ser	Leu	Leu	Gly	Gly	Glu	Gly	His	Phe	Ser	Lys	Asp	Val	His
	80								85					90
Leu	Pro	His	Asn	Tyr	His	Ile	Asp	Phe	Glu	Ile	Arg	Met	Asp	Thr
	95								100					105
Asn	Arg	Asn	Gln	Val	Leu	Pro	Leu	Ser	Asp	Val	Asp	Thr	Thr	Ser
	110								115					120
Ala	Thr	Asp	Ile	Gln	Arg	Val	Ala	Val	Leu	Cys	Val	Ser	Arg	Ser
	125								130					135
Ala	Tyr	Cys	Leu	Gly	Ser	Ser	His	Pro	Arg	Gly	Phe	Leu	Ala	Met
	140								145					150
Lys	Met	Arg	His	Leu	Asn	Ala	Met	Gly	Phe	His	Val	Ile	Leu	Val
	155								160					165
Asn	Asn	Trp	Glu	Met	Asp	Lys	Leu	Glu	Met	Glu	Asp	Ala	Val	Thr
	170								175					180
Phe	Leu	Lys	Thr	Lys	Ile	Tyr	Ser	Val	Glu	Ala	Leu	Pro	Val	Ala
	185								190					195
Ala	Val	Asn	Val	Gln	Ser	Thr	Gln							
	200													

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGAST01
- (B) CLONE: 1988911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45 :

Met	Glu	Arg	Gly	Asn	Val	Leu	Ser	Arg	Ala	Pro	Ser	Arg	Ala	His
5										10				15
Gly	Thr	His	Phe	Gly	Asp	Asp	Arg	Phe	Glu	Asp	Leu	Glu	Glu	Ala
	20								25					30
Asn	Pro	Phe	Ser	Phe	Arg	Glu	Phe	Leu	Lys	Thr	Lys	Asn	Leu	Gly
	35								40					45
Leu	Ser	Lys	Glu	Asp	Pro	Ala	Ser	Arg	Ile	Tyr	Ala	Lys	Glu	Ala
	50								55					60
Ser	Arg	His	Ser	Leu	Gly	Leu	Asp	His	Asn	Ser	Pro	Pro	Ser	Gln
	65								70					75
Thr	Gly	Gly	Tyr	Gly	Leu	Glu	Tyr	Gln	Gln	Pro	Phe	Glu	Asp	

80	85	90
Pro Thr Gly Ala Gly Asp Leu Leu Asp	Glu Glu Glu Asp Glu Asp	
95	100	105
Thr Gly Trp Ser Gly Ala Tyr Leu Pro	Ser Ala Ile Glu Gln Thr	
110	115	120
His Pro Glu Arg Val Pro Ala Gly Thr	Ser Pro Cys Ser Thr Tyr	
125	130	135
Leu Ser Phe Phe Ser Thr Pro Ser Glu	Leu Ala Gly Pro Glu Ser	
140	145	150
Leu Pro Ser Trp Ala Leu Ser Asp Thr	Asp Ser Arg Val Ser Pro	
155	160	165
Ala Ser Pro Ala Gly Ser Pro Ser Ala	Asp Phe Ala Val His Gly	
170	175	180
Glu Ser Leu Gly Asp Arg His Leu Arg	Thr Leu Gln Ile Ser Tyr	
185	190	195
Asp Ala Leu Lys Asp Glu Asn Ser Lys	Leu Arg Arg Lys Leu Asn	
200	205	210
Glu Val Gln Ser Phe Ser Glu Ala Gln	Thr Glu Met Val Arg Thr	
215	220	225
Leu Glu Arg Lys Leu Glu Ala Lys Met	Ile Lys Glu Glu Ser Asp	
230	235	240
Tyr His Asp Leu Glu Ser Val Val Gln	Gln Val Glu Gln Asn Leu	
245	250	255
Glu Leu Met Thr Lys Arg Ala Val Lys	Ala Glu Asn His Val Val	
260	265	270
Lys Leu Lys Gln Glu Ile Ser Leu Leu	Gln Ala Gln Val Ser Asn	
275	280	285
Phe Gln Arg Glu Asn Glu Ala Leu Arg	Cys Gly Gln Gly Ala Ser	
290	295	300
Leu Thr Val Val Lys Gln Asn Ala Asp	Val Ala Leu Gln Asn Leu	
305	310	315
Arg Val Val Met Asn Ser Ala Gln Ala	Ser Ile Lys Gln Leu Val	
320	325	330
Ser Gly Ala Glu Thr Leu Asn Leu Val	Ala Glu Ile Leu Lys Ser	
335	340	345
Ile Asp Arg Ile Ser Glu Val Lys Asp	Glu Glu Glu Asp Ser	
350	355	

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: OVARNOT03
 - (B) CLONE: 2061561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46 :

Met Gly Gly Lys Pro His Lys Glu Pro Arg Ala Lys Gly Pro Leu		
5	10	15
Ser Ile Phe Tyr Pro Gly Ser Thr Ala Pro Val Ile Thr Gln Arg		
20	25	30
Thr Pro Xaa Ala Ala Leu Lys Pro Pro Pro Ile Lys Gly Ala Gly		
35	40	45

Pro	Thr	Ile	Ala	Pro	Ile	Lys	Gly	Xaa	Xaa	Asn	Phe	Gly	Lys	Arg
50						55					60			
Pro	Thr	Val	Thr	Xaa	Pro	Xaa	Trp	Xaa	Ile	Ser	Pro	Asn	Trp	Gly
65							70				75			
Lys	Arg	Gly	Xaa	Cys	Xaa	Xaa	Xaa	Gly	Ile	Lys	Trp	Val	Xaa	Pro
80								85			90			
Arg	Val	Ser	Gln	Ala	Arg	Thr	Phe	Lys	Thr	Thr	Ala	Asn	Glu	Leu
95								100			105			
Xaa	Phe	Xaa	Asp	Thr	Phe	Glu	Glu	Xaa	Xaa	Arg	Xaa	Xaa	His	Ala
110								115			120			
Xaa	Val	Ser	Xaa	Glu	Pro	Gln	Pro	Arg	Cys	Pro	Leu	Gly	Glu	Ser
125								130			135			
Arg	Ser	Leu	Gly	Ala	Ala	Val	Cys	Arg	Trp	Asp	Ser	Phe	Asp	Phe
140								145			150			

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PANCNOT04
- (B) CLONE: 2084489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47 :

Met	Pro	Pro	Val	Ser	Arg	Ser	Ser	Tyr	Ser	Glu	Asp	Ile	Val	Gly
5								10				15		
Ser	Arg	Arg	Arg	Arg	Arg	Ser	Ser	Ser	Gly	Ser	Pro	Pro	Ser	Pro
								20			25			30
Gln	Ser	Arg	Cys	Ser	Ser	Trp	Asp	Gly	Cys	Ser	Arg	Ser	His	Ser
								35			40			45
Arg	Gly	Arg	Gly	Leu	Arg	Pro	Pro	Trp	Ser	Glu	Leu	Asp	Val	
				50				55			60			
Gly	Ala	Leu	Tyr	Pro	Phe	Ser	Arg	Ser	Gly	Ser	Arg	Gly	Arg	Leu
								65			70			75
Pro	Arg	Phe	Arg	Asn	Tyr	Ala	Phe	Ala	Ser	Ser	Trp	Ser	Thr	Ser
				80				85			90			
Tyr	Ser	Gly	Tyr	Arg	Tyr	His	Arg	His	Cys	Tyr	Ala	Glu	Glu	Arg
				95				100			105			
Gln	Ser	Ala	Glu	Asp	Tyr	Glu	Lys	Glu	Glu	Ser	His	Arg	Gln	Arg
				110				115			120			
Arg	Leu	Lys	Glu	Arg	Glu	Arg	Ile	Gly	Glu	Leu	Gly	Ala	Pro	Glu
				125				130			135			
Val	Trp	Gly	Pro	Ser	Pro	Lys	Phe	Pro	Gln	Leu	Asp	Ser	Asp	Glu
				140				145			150			
His	Thr	Pro	Val	Glu	Asp	Glu	Glu	Val	Thr	His	Gln	Lys	Ser	
				155				160			165			
Ser	Ser	Ser	Asp	Ser	Asn	Ser	Glu	Glu	His	Arg	Lys	Lys	Lys	Thr
				170				175			180			
Ser	Arg	Ser	Arg	Asn	Lys	Lys	Lys	Arg	Lys	Asn	Lys	Ser	Ser	Lys
				185				190			195			
Arg	Lys	His	Arg	Lys	Tyr	Ser	Asp	Ser	Asn	Ser	Glu	Ser		

	200	205	210											
Asp	Thr	Asn	Ser	Asp	Ser	Asp	Asp	Asp	Lys	Lys	Arg	Val	Lys	Ala
	215								220					225
Lys	His	Lys	Thr	Lys	Lys	Lys	Lys							
	230								235					240
Asn	Lys	Lys	Thr	Lys	Lys	Glu	Ser	Ser	Asp	Ser	Ser	Cys	Lys	Asp
	245								250					255
Ser	Glu	Glu	Asp	Leu	Ser	Glu	Ala	Thr	Trp	Met	Glu	Gln	Pro	Asn
	260								265					270
Val	Ala	Asp	Thr	Met	Asp	Leu	Ile	Gly	Pro	Glu	Ala	Pro	Ile	Ile
	275								280					285
His	Thr	Ser	Gln	Asp	Glu	Lys	Pro	Leu	Lys	Tyr	Gly	His	Ala	Leu
	290								295					300
Leu	Pro	Gly	Glu	Gly	Ala	Ala	Met	Ala	Glu	Tyr	Val	Lys	Ala	Gly
	305								310					315
Lys	Arg	Ile	Pro	Arg	Arg	Gly	Glu	Ile	Gly	Leu	Thr	Ser	Glu	Glu
	320								325					330
Ile	Gly	Ser	Phe	Glu	Cys	Ser	Gly	Tyr	Val	Met	Ser	Gly	Ser	Arg
	335								340					345
His	Arg	Arg	Met	Glu	Ala	Val	Arg	Leu	Arg	Lys	Glu	Asn	Gln	Ile
	350								355					360
Tyr	Ser	Ala	Asp	Glu	Lys	Arg	Ala	Leu	Ala	Ser	Phe	Asn	Gln	Glu
	365								370					375
Glu	Arg	Arg	Lys	Arg	Glu	Ser	Lys	Ile	Leu	Ala	Ser	Phe	Arg	Glu
	380								385					390
Met	Val	His	Lys	Lys	Thr	Lys	Glu	Lys	Asp	Asp	Asp	Lys		
	395								400					

(2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 311 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: SPLNFET02
 - (B) CLONE: 2203226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48 :

Met	His	Pro	Ala	Gly	Leu	Ala	Ala	Ala	Ala	Gly	Thr	Pro	Arg	
				5				10					15	
Leu	Pro	Ser	Lys	Arg	Arg	Ile	Pro	Val	Ser	Gln	Pro	Gly	Met	Ala
				20				25					30	
Asp	Pro	His	Gln	Leu	Phe	Asp	Asp	Thr	Ser	Ser	Ala	Gln	Ser	Arg
				35				40					45	
Gly	Tyr	Gly	Ala	Gln	Arg	Ala	Pro	Gly	Gly	Leu	Ser	Tyr	Pro	Ala
				50				55					60	
Ala	Ser	Pro	Thr	Pro	His	Ala	Ala	Phe	Leu	Ala	Asp	Pro	Val	Ser
				65				70					75	
Asn	Met	Ala	Met	Ala	Tyr	Gly	Ser	Ser	Leu	Ala	Ala	Gln	Gly	Lys
				80				85					90	
Glu	Leu	Val	Asp	Lys	Asn	Ile	Asp	Arg	Phe	Ile	Pro	Ile	Thr	Lys
				95				100					105	
Leu	Lys	Tyr	Tyr	Phe	Ala	Val	Asp	Thr	Met	Tyr	Val	Gly	Arg	Lys
				110				115					120	

Leu	Gly	Leu	Leu	Phe	Phe	Pro	Tyr	Leu	His	Gln	Asp	Trp	Glu	Val
				125					130					135
Gln	Tyr	Gln	Gln	Asp	Thr	Pro	Val	Ala	Pro	Arg	Phe	Asp	Val	Asn
				140					145					150
Ala	Pro	Asp	Leu	Tyr	Ile	Pro	Ala	Met	Ala	Phe	Ile	Thr	Tyr	Val
				155					160					165
Leu	Val	Ala	Gly	Leu	Ala	Leu	Gly	Thr	Gln	Asp	Arg	Phe	Ser	Pro
				170					175					180
Asp	Leu	Leu	Gly	Leu	Gln	Ala	Ser	Ser	Ala	Leu	Ala	Trp	Leu	Thr
				185					190					195
Leu	Glu	Val	Leu	Ala	Ile	Leu	Leu	Ser	Leu	Tyr	Leu	Val	Thr	Val
				200					205					210
Asn	Thr	Asp	Leu	Thr	Thr	Ile	Asp	Leu	Val	Ala	Phe	Leu	Gly	Tyr
				215					220					225
Lys	Tyr	Val	Gly	Met	Ile	Gly	Gly	Val	Leu	Met	Gly	Leu	Leu	Phe
				230					235					240
Gly	Lys	Ile	Gly	Tyr	Tyr	Leu	Val	Leu	Gly	Trp	Cys	Cys	Val	Ala
				245					250					255
Ile	Phe	Val	Phe	Met	Ile	Arg	Thr	Leu	Arg	Leu	Lys	Ile	Leu	Ala
				260					265					270
Asp	Ala	Ala	Ala	Glu	Gly	Val	Pro	Val	Arg	Gly	Ala	Arg	Asn	Gln
				275					280					285
Leu	Arg	Met	Tyr	Leu	Thr	Met	Ala	Val	Ala	Ala	Ala	Gln	Pro	Met
				290					295					300
Leu	Met	Tyr	Trp	Leu	Thr	Phe	His	Leu	Val	Arg				
				305					310					

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT16
- (B) CLONE: 2232884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49 :

Met	Ala	Ser	Ala	Asp	Glu	Leu	Thr	Phe	His	Glu	Phe	Glu	Glu	Ala
				5					10					15
Thr	Asn	Leu	Leu	Ala	Asp	Thr	Pro	Asp	Ala	Ala	Thr	Thr	Ser	Arg
				20					25					30
Ser	Asp	Gln	Leu	Thr	Pro	Gln	Gly	His	Val	Ala	Val	Ala	Val	Gly
				35					40					45
Ser	Gly	Gly	Ser	Tyr	Gly	Ala	Glu	Asp	Glu	Val	Glu	Glu	Glu	Ser
				50					55					60
Asp	Lys	Ala	Ala	Leu	Leu	Gln	Glu	Gln	Gln	Gln	Gln	Gln	Pro	
				65					70					75
Gly	Phe	Trp	Thr	Phe	Ser	Tyr	Tyr	Gln	Ser	Phe	Phe	Asp	Val	Asp
				80					85					90
Thr	Ser	Gln	Val	Leu	Asp	Arg	Ile	Lys	Gly	Ser	Leu	Leu	Pro	Arg
				95					100					105
Pro	Gly	His	Asn	Phe	Val	Arg	His	His	Leu	Arg	Asn	Arg	Pro	Asp
				110					115					120
Leu	Tyr	Gly	Pro	Phe	Trp	Ile	Cys	Ala	Thr	Leu	Ala	Phe	Val	Leu

125		130		135										
Ala	Val	Thr	Gly	Asn	Leu	Thr	Leu	Val	Leu	Ala	Gln	Arg	Arg	Asp
				140					145					150
Pro	Ser	Ile	His	Tyr	Ser	Pro	Gln	Phe	His	Lys	Val	Thr	Val	Ala
				155					160					165
Gly	Ile	Ser	Ile	Tyr	Cys	Tyr	Ala	Trp	Leu	Val	Pro	Leu	Ala	Leu
				170					175					180
Trp	Gly	Phe	Leu	Arg	Trp	Arg	Lys	Gly	Val	Gln	Glu	Arg	Met	Gly
				185					190					195
Pro	Tyr	Thr	Phe	Leu	Glu	Thr	Val	Cys	Ile	Tyr	Gly	Tyr	Ser	Leu
				200					205					210
Phe	Val	Phe	Ile	Pro	Met	Val	Val	Leu	Trp	Leu	Ile	Pro	Val	Pro
				215					220					225
Trp	Leu	Gln	Trp	Leu	Phe	Gly	Ala	Leu	Ala	Leu	Gly	Leu	Ser	Ala
				230					235					240
Ala	Gly	Leu	Val	Phe	Thr	Leu	Trp	Pro	Val	Val	Arg	Glu	Asp	Thr
				245					250					255
Arg	Leu	Val	Ala	Thr	Val	Leu	Leu	Ser	Val	Val	Val	Leu	Leu	His
				260					265					270
Ala	Leu	Leu	Ala	Met	Gly	Cys	Lys	Leu	Tyr	Phe	Phe	Gln	Ser	Leu
				275					280					285
Pro	Pro	Glu	Asn	Val	Ala	Pro	Pro	Pro	Gln	Ile	Thr	Ser	Leu	Pro
				290					295					300
Ser	Asn	Ile	Ala	Leu	Ser	Pro	Thr	Leu	Pro	Gln	Ser	Leu	Ala	Pro
				305					310					315
Ser														

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT11
- (B) CLONE: 2328134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50 :

Met	Thr	Pro	Arg	Thr	Trp	Trp	Pro	Arg	Pro	Ala	Gly	Trp	Gly	Thr
				5					10					15
Cys	Arg	Ala	Ala	Gly	Trp	Pro	Arg	Ser	Val	Pro	Trp	Ala	Arg	Thr
				20					25					30
Ala	Ala	Ser	Leu	Val	Phe	Val	Pro	Thr	Arg	Arg	Arg	Ser	Gly	Pro
				35					40					45
Ser	Gly	Thr	Ala	Ser	Val	Ala	Ala	Met	Ala	Tyr	His	Ser	Gly	Tyr
				50					55					60
Gly	Ala	His	Gly	Ser	Lys	His	Arg	Ala	Arg	Ala	Ala	Pro	Asp	Pro
				65					70					75
Pro	Pro	Leu	Phe	Asp	Asp	Thr	Ser	Gly	Gly	Tyr	Ser	Ser	Gln	Pro
				80					85					90
Gly	Gly	Tyr	Pro	Ala	Thr	Gly	Ala	Asp	Val	Ala	Phe	Ser	Val	Asn
				95					100					105
His	Leu	Leu	Gly	Asp	Pro	Met	Ala	Asn	Val	Ala	Met	Ala	Tyr	Gly
				110					115					120
Ser	Ser	Ile	Ala	Ser	His	Gly	Lys	Asp	Met	Val	His	Lys	Glu	Leu
				125					130					135

His	Arg	Phe	Val	Ser	Val	Ser	Lys	Leu	Lys	Tyr	Phe	Phe	Ala	Val
					140				145					150
Asp	Thr	Ala	Tyr	Val	Ala	Lys	Lys	Leu	Gly	Leu	Leu	Val	Phe	Pro
					155				160					165
Tyr	Thr	His	Gln	Asn	Trp	Glu	Val	Gln	Tyr	Ser	Arg	Asp	Ala	Pro
					170				175					180
Leu	Pro	Pro	Arg	Gln	Asp	Leu	Asn	Ala	Pro	Asp	Leu	Tyr	Ile	Pro
					185				190					195
Thr	Met	Ala	Phe	Ile	Thr	Tyr	Val	Leu	Leu	Ala	Gly	Met	Ala	Leu
					200				205					210
Gly	Ile	Gln	Lys	Arg	Phe	Ser	Pro	Glu	Val	Leu	Gly	Leu	Cys	Ala
					215				220					225
Ser	Thr	Ala	Leu	Val	Trp	Val	Val	Met	Glu	Val	Leu	Ala	Leu	Leu
					230				235					240
Leu	Gly	Leu	Tyr	Leu	Ala	Thr	Val	Arg	Ser	Asp	Leu	Ser	Thr	Phe
					245				250					255
His	Leu	Leu	Ala	Tyr	Ser	Gly	Tyr	Lys	Tyr	Val	Gly	Met	Ile	Leu
					260				265					270
Ser	Val	Leu	Thr	Gly	Leu	Leu	Phe	Gly	Ser	Asp	Gly	Tyr	Tyr	Val
					275				280					285
Ala	Leu	Ala	Trp	Thr	Ser	Ser	Ala	Leu	Met	Tyr	Phe	Ile	Val	Arg
					290				295					300
Ser	Leu	Arg	Thr	Ala	Ala	Leu	Gly	Pro	Asp	Ser	Met	Gly	Gly	Pro
					305				310					315
Val	Pro	Arg	Gln	Arg	Leu	Gln	Leu	Tyr	Leu	Thr	Leu	Gly	Ala	Ala
					320				325					330
Ala	Phe	Gln	Pro	Leu	Ile	Ile	Tyr	Trp	Leu	Thr	Phe	His	Leu	Val
					335				340					345

Arg

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 299 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: ISLTNOT01
 - (B) CLONE: 2382718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51 :

Met	Gly	Thr	Lys	Ala	Gln	Val	Glu	Arg	Lys	Leu	Leu	Cys	Leu	Phe
						5			10					15
Ile	Leu	Ala	Ile	Leu	Leu	Cys	Ser	Leu	Ala	Leu	Gly	Ser	Val	Thr
						20			25					30
Val	His	Ser	Ser	Glu	Pro	Glu	Val	Arg	Ile	Pro	Glu	Asn	Asn	Pro
					35				40					45
Val	Lys	Leu	Ser	Cys	Ala	Tyr	Ser	Gly	Phe	Ser	Ser	Pro	Arg	Val
					50				55					60
Glu	Trp	Lys	Phe	Asp	Gln	Gly	Asp	Thr	Thr	Arg	Leu	Val	Cys	Tyr
					65				70					75
Asn	Asn	Lys	Ile	Thr	Ala	Ser	Tyr	Glu	Asp	Arg	Val	Thr	Phe	Leu
					80				85					90
Pro	Thr	Gly	Ile	Thr	Phe	Lys	Ser	Val	Thr	Arg	Glu	Asp	Thr	Gly
					95				100					105
Thr	Tyr	Thr	Cys	Met	Val	Ser	Glu	Glu	Gly	Asn	Ser	Tyr	Gly	

	110		115		120									
Glu	Val	Lys	Val	Lys	Leu	Ile	Val	Leu	Val	Pro	Pro	Ser	Lys	Pro
	125								130					135
Thr	Val	Asn	Ile	Pro	Ser	Ser	Ala	Thr	Ile	Gly	Asn	Arg	Ala	Val
	140								145					150
Leu	Thr	Cys	Ser	Glu	Gln	Asp	Gly	Ser	Pro	Pro	Ser	Glu	Tyr	Thr
	155								160					165
Trp	Phe	Lys	Asp	Gly	Ile	Val	Met	Pro	Thr	Asn	Pro	Lys	Ser	Thr
	170								175					180
Arg	Ala	Phe	Ser	Asn	Ser	Ser	Tyr	Val	Leu	Asn	Pro	Thr	Thr	Gly
	185								190					195
Glu	Leu	Val	Phe	Asp	Pro	Leu	Ser	Ala	Ser	Asp	Thr	Gly	Glu	Tyr
	200								205					210
Ser	Cys	Glu	Ala	Arg	Asn	Gly	Tyr	Gly	Thr	Pro	Met	Thr	Ser	Asn
	215								220					225
Ala	Val	Arg	Met	Glu	Ala	Val	Glu	Arg	Asn	Val	Gly	Val	Ile	Val
	230								235					240
Ala	Ala	Val	Leu	Val	Thr	Leu	Ile	Leu	Leu	Gly	Ile	Leu	Val	Phe
	245								250					255
Gly	Ile	Trp	Phe	Ala	Tyr	Ser	Arg	Gly	His	Phe	Asp	Arg	Thr	Lys
	260								265					270
Lys	Gly	Thr	Ser	Ser	Lys	Lys	Val	Ile	Tyr	Ser	Gln	Pro	Ser	Ala
	275								280					285
Arg	Ser	Glu	Gly	Glu	Phe	Lys	Gln	Thr	Ser	Ser	Phe	Leu	Val	
	290								295					

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: ENDANOT01
- (B) CLONE: 2452208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52 :

Met	Ala	Ser	Thr	Gly	Ser	Gln	Ala	Ser	Asp	Ile	Asp	Glu	Ile	Phe
										5	10			15
Gly	Phe	Phe	Asn	Asp	Gly	Glu	Pro	Pro	Thr	Lys	Lys	Pro	Arg	Lys
										20	25			30
Leu	Leu	Pro	Ser	Leu	Lys	Thr	Lys	Lys	Pro	Arg	Glu	Leu	Val	Leu
										35	40			45
Val	Ile	Gly	Thr	Gly	Ile	Ser	Ala	Ala	Val	Ala	Pro	Gln	Val	Pro
										50	55			60
Ala	Leu	Lys	Ser	Trp	Lys	Gly	Leu	Ile	Gln	Ala	Leu	Leu	Asp	Ala
										65	70			75
Ala	Ile	Asp	Phe	Asp	Leu	Leu	Glu	Asp	Glu	Glu	Ser	Lys	Lys	Phe
										80	85			90
Gln	Lys	Cys	Leu	His	Glu	Asp	Lys	Asn	Leu	Val	His	Val	Ala	His
										95	100			105
Asp	Leu	Ile	Gln	Lys	Leu	Ser	Pro	Arg	Thr	Ser	Asn	Val	Arg	Ser
										110	115			120
Thr	Phe	Phe	Lys	Asp	Cys	Leu	Tyr	Glu	Val	Phe	Asp	Asp	Leu	Glu
										125	130			135

Ser	Lys	Met	Glu	Asp	Ser	Gly	Lys	Gln	Leu	Leu	Gln	Ser	Val	Leu
									140	145				150
His	Leu	Met	Glu	Asn	Gly	Ala	Leu	Val	Leu	Thr	Thr	Asn	Phe	Asp
									155	160				165
Asn	Leu	Leu	Glu	Leu	Tyr	Ala	Ala	Asp	Gln	Gly	Lys	Gln	Leu	Glu
									170	175				180
Ser	Leu	Asp	Leu	Thr	Asp	Glu	Lys	Lys	Val	Leu	Glu	Trp	Ala	Gln
									185	190				195
Glu	Lys	Arg	Lys	Leu	Ser	Val	Leu	His	Ile	His	Gly	Val	Tyr	Thr
									200	205				210
Asn	Pro	Ser	Gly	Ile	Val	Leu	His	Pro	Ala	Gly	Tyr	Gln	Asn	Val
									215	220				225
Leu	Arg	Asn	Thr	Glu	Val	Met	Arg	Glu	Ile	Gln	Lys	Leu	Tyr	Glu
									230	235				240
Asn	Lys	Ser	Phe	Leu	Phe	Leu	Gly	Cys	Gly	Trp	Thr	Val	Asp	Asp
									245	250				255
Thr	Thr	Phe	Gln	Ala	Leu	Phe	Leu	Glu	Ala	Val	Lys	His	Lys	Ser
									260	265				270
Asp	Leu	Glu	His	Phe	Met	Leu	Val	Arg	Arg	Gly	Asp	Val	Asp	Glu
									275	280				285
Phe	Lys	Lys	Leu	Arg	Glu	Asn	Met	Leu	Asp	Lys	Gly	Ile	Lys	Val
									290	295				300
Ile	Ser	Tyr	Gly	Asp	Asp	Tyr	Ala	Asp	Leu	Pro	Glu	Tyr	Phe	Lys
									305	310				315
Arg	Leu	Thr	Cys	Glu	Ile	Ser	Thr	Arg	Gly	Thr	Ser	Ala	Gly	Met
									320	325				330
Val	Arg	Glu	Gly	Gln	Leu	Asn	Gly	Ser	Ser	Ala	Ala	His	Ser	Glu
									335	340				345
Ile	Arg	Gly	Cys	Ser	Thr									
						350								

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 662 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: ENDANOT01
 - (B) CLONE: 2457825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53 :

Met	Thr	Ala	Lys	Lys	Gln	Cys	Leu	Leu	Arg	Leu	Gly	Val	Leu	Arg
							5		10				15	
Gln	Asp	Trp	Pro	Asp	Thr	Asn	Arg	Leu	Leu	Gly	Ser	Ala	Asn	Val
								20	25				30	
Val	Pro	Glu	Ala	Leu	Gln	Arg	Phe	Thr	Arg	Ala	Ala	Ala	Asp	Phe
								35	40				45	
Ala	Thr	His	Gly	Lys	Leu	Gly	Lys	Leu	Glu	Phe	Ala	Gln	Asp	Ala
								50	55				60	
His	Gly	Gln	Pro	Asp	Val	Ser	Ala	Phe	Asp	Phe	Thr	Ser	Met	Met
								65	70				75	
Arg	Ala	Glu	Ser	Ser	Ala	Arg	Val	Gln	Glu	Lys	His	Gly	Ala	Arg
								80	85				90	
Leu	Leu	Leu	Gly	Leu	Val	Gly	Asp	Cys	Leu	Val	Glu	Pro	Phe	Trp

	95		100		105									
Pro	Leu	Gly	Thr	Gly	Val	Ala	Arg	Gly	Phe	Leu	Ala	Ala	Phe	Asp
					110				115					120
Ala	Ala	Trp	Met	Val	Lys	Arg	Trp	Ala	Glu	Gly	Ala	Glu	Ser	Leu
					125				130					135
Glu	Val	Leu	Ala	Glu	Arg	Glu	Ser	Leu	Tyr	Gln	Leu	Leu	Ser	Gln
					140				145					150
Thr	Ser	Pro	Glu	Asn	Met	His	Arg	Asn	Val	Ala	Gln	Tyr	Gly	Leu
					155				160					165
Asp	Pro	Ala	Thr	Arg	Tyr	Pro	Asn	Leu	Asn	Leu	Arg	Ala	Val	Thr
					170				175					180
Pro	Asn	Gln	Val	Arg	Asp	Leu	Tyr	Asp	Val	Leu	Ala	Lys	Glu	Pro
					185				190					195
Val	Gln	Arg	Asp	Asn	Asp	Lys	Thr	Asp	Thr	Gly	Met	Pro	Ala	Thr
					200				205					210
Gly	Ser	Ala	Gly	Thr	Gln	Glu	Glu	Leu	Leu	Arg	Trp	Cys	Gln	Glu
					215				220					225
Gln	Thr	Ala	Gly	Tyr	Pro	Gly	Val	His	Val	Ser	Asp	Leu	Ser	Ser
					230				235					240
Ser	Trp	Ala	Asp	Gly	Leu	Ala	Leu	Cys	Ala	Leu	Val	Tyr	Arg	Leu
					245				250					255
Gln	Pro	Gly	Leu	Leu	Glu	Pro	Ser	Glu	Leu	Gln	Gly	Leu	Gly	Ala
					260				265					270
Leu	Glu	Ala	Thr	Ala	Trp	Ala	Leu	Lys	Val	Ala	Glu	Asn	Glu	Leu
					275				280					285
Gly	Ile	Thr	Pro	Val	Val	Ser	Ala	Gln	Ala	Val	Val	Ala	Gly	Ser
					290				295					300
Asp	Pro	Leu	Gly	Leu	Ile	Ala	Tyr	Leu	Ser	His	Phe	His	Ser	Ala
					305				310					315
Phe	Lys	Ser	Met	Ala	His	Ser	Pro	Gly	Pro	Val	Ser	Gln	Ala	Ser
					320				325					330
Pro	Gly	Thr	Ser	Ser	Ala	Val	Leu	Phe	Leu	Ser	Lys	Leu	Gln	Arg
					335				340					345
Thr	Leu	Gln	Arg	Ser	Arg	Ala	Lys	Glu	Asn	Ala	Glu	Asp	Ala	Gly
					350				355					360
Gly	Lys	Lys	Leu	Arg	Leu	Glu	Met	Glu	Ala	Glu	Thr	Pro	Ser	Thr
					365				370					375
Glu	Val	Pro	Pro	Asp	Pro	Glu	Pro	Gly	Val	Pro	Leu	Thr	Pro	Pro
					380				385					390
Ser	Gln	His	Gln	Glu	Ala	Gly	Ala	Gly	Asp	Leu	Cys	Ala	Leu	Cys
					395				400					405
Gly	Glu	His	Leu	Tyr	Val	Leu	Glu	Arg	Leu	Cys	Val	Asn	Gly	His
					410				415					420
Phe	Phe	His	Arg	Ser	Cys	Phe	Arg	Cys	His	Thr	Cys	Glu	Ala	Thr
					425				430					435
Leu	Trp	Pro	Gly	Gly	Tyr	Glu	Gln	His	Pro	Gly	Ser	Arg	Thr	Ser
					440				445					450
Gln	Phe	Phe	Phe	Ser	Ala	Leu	Val	Ala	Met	Glu	Lys	Glu	Glu	Lys
					455				460					465
Glu	Ser	Pro	Phe	Ser	Ser	Glu	Glu	Glu	Glu	Glu	Asp	Val	Pro	Leu
					470				475					480
Asp	Ser	Asp	Val	Glu	Gln	Ala	Leu	Gln	Thr	Phe	Ala	Lys	Thr	Ser
					485				490					495
Gly	Thr	Met	Asn	Asn	Tyr	Pro	Thr	Trp	Arg	Arg	Thr	Leu	Leu	Arg
					500				505					510
Arg	Ala	Lys	Glu	Glu	Glu	Met	Lys	Arg	Phe	Cys	Lys	Ala	Gln	Thr
					515				520					525
Ile	Gln	Arg	Arg	Leu	Asn	Glu	Ile	Glu	Ala	Ala	Leu	Arg	Glu	Leu
					530				535					540
Glu	Ala	Glu	Gly	Val	Lys	Leu	Glu	Leu	Ala	Leu	Arg	Arg	Gln	Ser
					545				550					555

Ser	Ser	Pro	Glu	Gln	Gln	Lys	Lys	Leu	Trp	Val	Gly	Gln	Leu	Leu
				560					565					570
Gln	Leu	Val	Asp	Lys	Lys	Asn	Ser	Leu	Val	Ala	Glu	Glu	Ala	Glu
				575					580					585
Leu	Met	Ile	Thr	Val	Gln	Glu	Leu	Asn	Leu	Glu	Glu	Lys	Gln	Trp
				590					595					600
Gln	Leu	Asp	Gln	Glu	Leu	Arg	Gly	Tyr	Met	Asn	Arg	Glu	Glu	Asn
				605					610					615
Leu	Lys	Thr	Ala	Ala	Asp	Arg	Gln	Ala	Glu	Asp	Gln	Val	Leu	Arg
				620					625					630
Lys	Leu	Val	Asp	Leu	Val	Asn	Gln	Arg	Asp	Ala	Leu	Ile	Arg	Phe
				635					640					645
Gln	Glu	Glu	Arg	Arg	Leu	Ser	Glu	Leu	Ala	Leu	Gly	Thr	Gly	Ala
				650					655					660
Gln	Gly													

(2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: THP1NOT03
 - (B) CLONE: 2470740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54 :

Met	Ala	Ser	Trp	Pro	Ala	Ser	Pro	Leu	Gln	Trp	Gly	Pro	Pro	Leu
				5					10					15
Ala	Ser	Cys	Pro	Ser	Cys	Cys	Cys	Cys	Phe	His	Cys	Trp	Gln	
					20				25					30
Pro	Arg	Val	Gly	Val	Ala	Cys	Arg	Gln	Cys	Trp	Pro	Leu	Arg	
					35				40					45
Trp	Gly	Trp	Trp	Val	Trp	Gly	Pro	Pro	Thr	Cys	Ser	Phe	Val	Gln
					50				55					60
Pro	Cys	Thr	Cys	Pro	Pro	Val	Phe	Ser	Tyr	Ser	Trp	Pro	Arg	Val
					65				70					75
Pro	His	Trp	Gly	Pro	Ser	Trp	Xaa	Met	Ser	Trp	Arg	Arg	Arg	Leu
					80				85					90
Met	Gly	Val	Pro	Leu	Gly	Leu	Trp	Asn	Cys	Leu	Val	Leu	Lys	Leu
					95				100					105
Xaa	Gln	Gly	Leu	Ala	Pro	Thr	Ser	Gly	Gly					
					110				115					

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:

(A) LIBRARY: SMCANOT01
 (B) CLONE: 2479092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55 :

Met Glu Ala Leu Arg Arg Ala His Glu Val Ala Leu Arg Leu Leu
 5 10 15
 Leu Cys Arg Pro Trp Ala Ser Arg Ala Ala Arg Pro Lys Pro
 20 25 30
 Ser Ala Ser Glu Val Leu Thr Arg His Leu Leu Gln Arg Arg Leu
 35 40 45
 Pro His Trp Thr Ser Phe Cys Val Pro Tyr Ser Ala Val Arg Asn
 50 55 60
 Asp Gln Phe Gly Leu Ser His Phe Asn Trp Pro Val Gln Gly Ala
 65 70 75
 Asn Tyr His Val Leu Arg Thr Gly Cys Phe Pro Phe Ile Lys Tyr
 80 85 90
 His Cys Ser Lys Ala Pro Trp Gln Asp Leu Ala Arg Gln Asn Arg
 95 100 105
 Phe Phe Thr Ala Leu Lys Val Val Asn Leu Gly Ile Pro Thr Leu
 110 115 120
 Leu Tyr Gly Leu Gly Ser Trp Leu Phe Ala Arg Val Thr Glu Thr
 125 130 135
 Val His Thr Ser Tyr Gly Pro Ile Thr Val Tyr Phe Leu Asn Lys
 140 145 150
 Glu Asp Glu Gly Ala Met Tyr
 155

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 197 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: SMCANOT01
 (B) CLONE: 2480544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56 :

Met Pro Pro Ala Gly Leu Arg Arg Ala Ala Pro Leu Thr Ala Ile
 5 10 15
 Ala Leu Leu Val Leu Gly Ala Pro Leu Val Leu Ala Gly Glu Asp
 20 25 30
 Cys Leu Trp Tyr Leu Asp Arg Asn Gly Ser Trp His Pro Gly Phe
 35 40 45
 Asn Cys Glu Phe Phe Cys Cys Gly Thr Cys Tyr His Arg
 50 55 60
 Tyr Cys Cys Arg Asp Leu Thr Leu Leu Ile Thr Glu Arg Gln Gln
 65 70 75
 Lys His Cys Leu Ala Phe Ser Pro Lys Thr Ile Ala Gly Ile Ala
 80 85 90
 Ser Ala Val Ile Leu Phe Val Ala Val Val Ala Thr Thr Ile Cys
 95 100 105
 Cys Phe Leu Cys Ser Cys Cys Tyr Leu Tyr Arg Arg Arg Gln Gln
 110 115 120

Leu	Gln	Ser	Pro	Phe	Glu	Gly	Gln	Glu	Ile	Pro	Met	Thr	Gly	Ile
				125					130					135
Pro	Val	Gln	Pro	Val	Tyr	Pro	Tyr	Pro	Gln	Asp	Pro	Lys	Ala	Gly
				140					145					150
Pro	Ala	Pro	Pro	Gln	Pro	Gly	Phe	Met	Tyr	Pro	Pro	Ser	Gly	Pro
				155					160					165
Ala	Pro	Gln	Tyr	Pro	Leu	Tyr	Pro	Ala	Gly	Pro	Pro	Val	Tyr	Asn
				170					175					180
Pro	Ala	Ala	Pro	Pro	Pro	Tyr	Met	Pro	Pro	Gln	Pro	Ser	Tyr	Pro
				185					190					195
														Gly Ala

(2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 245 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: BRAITUT21
 - (B) CLONE: 2518547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57 :

Met	Gly	Gly	Ala	Ser	Arg	Arg	Val	Glu	Ser	Gly	Ala	Trp	Ala	Tyr
					5			10						15
Leu	Ser	Pro	Leu	Val	Leu	Arg	Lys	Glu	Leu	Glu	Ser	Leu	Val	Glu
					20			25						30
Asn	Glu	Gly	Ser	Glu	Val	Leu	Ala	Leu	Pro	Glu	Leu	Pro	Ser	Ala
					35			40						45
His	Pro	Ile	Ile	Phe	Trp	Asn	Leu	Leu	Trp	Tyr	Phe	Gln	Arg	Leu
					50			55						60
Arg	Leu	Pro	Ser	Ile	Leu	Pro	Gly	Leu	Val	Leu	Ala	Ser	Cys	Asp
					65			70						75
Gly	Pro	Ser	His	Ser	Gln	Ala	Pro	Ser	Pro	Trp	Leu	Thr	Pro	Asp
					80			85						90
Pro	Ala	Ser	Val	Gln	Val	Arg	Leu	Leu	Trp	Asp	Val	Leu	Thr	Pro
					95			100						105
Asp	Pro	Asn	Ser	Cys	Pro	Pro	Leu	Tyr	Val	Leu	Trp	Arg	Val	His
					110			115						120
Ser	Gln	Ile	Pro	Gln	Arg	Val	Val	Trp	Pro	Gly	Pro	Val	Pro	Ala
					125			130						135
Ser	Leu	Ser	Leu	Ala	Leu	Leu	Glu	Ser	Val	Leu	Arg	His	Val	Gly
					140			145						150
Leu	Asn	Glu	Val	His	Lys	Ala	Val	Gly	Leu	Leu	Leu	Glu	Thr	Leu
					155			160						165
Gly	Pro	Pro	Pro	Thr	Gly	Leu	His	Leu	Gln	Arg	Gly	Ile	Tyr	Arg
					170			175						180
Glu	Ile	Leu	Phe	Leu	Thr	Met	Ala	Ala	Leu	Gly	Lys	Asp	His	Val
					185			190						195
Asp	Ile	Val	Ala	Phe	Asp	Lys	Lys	Tyr	Lys	Ser	Ala	Phe	Asn	Lys
					200			205						210
Leu	Ala	Ser	Ser	Met	Gly	Lys	Glu	Glu	Leu	Arg	His	Arg	Arg	Ala
					215			220						225
Gln	Met	Pro	Thr	Pro	Lys	Ala	Ile	Asp	Cys	Arg	Lys	Cys	Phe	Gly
					230			235						240

Ala Pro Pro Glu Cys
245

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GBLANOT02
- (B) CLONE: 2530650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58 :

Met	Leu	Leu	Pro	Gln	Leu	Cys	Trp	Leu	Pro	Leu	Leu	Ala	Gly	Leu
														15
5														
Leu	Pro	Pro	Val	Pro	Ala	Gln	Lys	Phe	Ser	Ala	Leu	Thr	Phe	Leu
														30
20														
Arg	Val	Asp	Gln	Asp	Lys	Asp	Lys	Asp	Cys	Ser	Leu	Asp	Cys	Ala
														45
35														
Gly	Ser	Pro	Gln	Lys	Pro	Leu	Cys	Ala	Ser	Asp	Gly	Arg	Thr	Phe
														60
50														
Leu	Ser	Arg	Cys	Glu	Phe	Gln	Arg	Ala	Lys	Cys	Lys	Asp	Pro	Gln
														75
65														
Leu	Glu	Ile	Ala	Tyr	Arg	Gly	Asn	Cys	Lys	Asp	Val	Ser	Arg	Cys
														90
80														
Val	Ala	Glu	Arg	Lys	Tyr	Thr	Gln	Glu	Gln	Ala	Arg	Lys	Glu	Phe
														105
95														
Gln	Gln	Val	Phe	Ile	Pro	Glu	Cys	Asn	Asp	Asp	Gly	Thr	Tyr	Ser
														120
110														
Gln	Val	Gln	Cys	His	Ser	Tyr	Thr	Gly	Tyr	Cys	Trp	Cys	Val	Thr
														135
125														
Pro	Asn	Gly	Arg	Pro	Ile	Ser	Gly	Thr	Ala	Val	Ala	His	Lys	Thr
														150
140														
Pro	Arg	Cys	Pro	Gly	Ser	Val	Asn	Glu	Lys	Leu	Pro	Gln	Arg	Glu
														165
155														
Gly	Thr	Gly	Lys	Thr	Asp	Asp	Ala	Ala	Ala	Pro	Ala	Leu	Glu	Thr
														180
170														
Gln	Pro	Gln	Gly	Asp	Glu	Glu	Asp	Ile	Ala	Ser	Arg	Tyr	Pro	Thr
														195
185														
Leu	Trp	Thr	Glu	Gln	Val	Lys	Ser	Arg	Gln	Asn	Lys	Thr	Asn	Lys
														210
200														
Asn	Ser	Val	Ser	Ser	Cys	Asp	Gln	Glu	His	Gln	Ser	Ala	Leu	Glu
														225
215														
Glu	Ala	Lys	Gln	Pro	Lys	Asn	Asp	Asn	Val	Val	Ile	Pro	Glu	Cys
														240
230														
Ala	His	Gly	Gly	Leu	Tyr	Lys	Pro	Val	Gln	Cys	His	Pro	Ser	Thr
														255
245														
Gly	Tyr	Cys	Trp	Cys	Val	Leu	Val	Asp	Thr	Gly	Arg	Pro	Ile	Pro
														270
260														
Gly	Thr	Ser	Thr	Arg	Tyr	Glu	Gln	Pro	Lys	Cys	Asp	Asn	Thr	Gly
														285
275														
Gln	Gly	Pro	Pro	Ser	Gln	Ser	Pro	Gly	Pro	Val	Gln	Gly	Pro	Pro
														300
290														
Ala	Thr	Arg	Leu	Ser	Gly	Cys	Gln	Lys	Ala					

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THYMNOT04
- (B) CLONE: 2652271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59 :

Met	Arg	Pro	Ala	Ala	Leu	Arg	Gly	Ala	Leu	Leu	Gly	Cys	Leu	Cys	
					5				10					15	
Leu	Ala	Leu	Leu	Cys	Leu	Gly	Gly	Ala	Asp	Lys	Arg	Leu	Arg	Asp	
					20				25					30	
Asn	His	Glu	Trp	Lys	Lys	Leu	Ile	Met	Val	Gln	His	Trp	Pro	Glu	
					35				40					45	
Thr	Val	Cys	Glu	Lys	Ile	Gln	Asn	Asp	Cys	Arg	Asp	Pro	Pro	Asp	
					50				55					60	
Tyr	Trp	Thr	Ile	His	Gly	Leu	Trp	Pro	Asp	Lys	Ser	Glu	Gly	Cys	
					65				70					75	
Asn	Arg	Ser	Trp	Pro	Phe	Asn	Leu	Glu	Ile	Lys	Asp	Leu	Leu		
					80				85					90	
Pro	Glu	Met	Arg	Ala	Tyr	Trp	Pro	Asp	Val	Ile	His	Ser	Phe	Pro	
					95				100					105	
Asn	Arg	Ser	Arg	Phe	Trp	Lys	His	Glu	Trp	Glu	Lys	His	Gly	Thr	
					110				115					120	
Cys	Ala	Ala	Gln	Val	Asp	Ala	Leu	Asn	Ser	Gln	Lys	Lys	Tyr	Phe	
					125				130					135	
Gly	Arg	Ser	Leu	Glu	Leu	Tyr	Arg	Glu	Leu	Asp	Leu	Asn	Ser	Val	
					140				145					150	
Leu	Leu	Lys	Leu	Gly	Ile	Lys	Pro	Ser	Ile	Asn	Tyr	Tyr	Gln	Val	
					155				160					165	
Ala	Asp	Phe	Lys	Asp	Ala	Leu	Ala	Arg	Val	Tyr	Gly	Val	Ile	Pro	
					170				175					180	
Lys	Ile	Gln	Cys	Leu	Pro	Pro	Ser	Gln	Asp	Glu	Glu	Val	Gln	Thr	
					185				190					195	
Ile	Gly	Gln	Ile	Glu	Leu	Cys	Leu	Thr	Lys	Gln	Asp	Gln	Gln	Leu	
					200				205					210	
Gln	Asn	Cys	Thr	Glu	Pro	Gly	Glu	Gln	Pro	Ser	Pro	Lys	Gln	Glu	
					215				220					225	
Val	Trp	Leu	Ala	Asn	Gly	Ala	Ala	Glu	Ser	Arg	Gly	Leu	Arg	Val	
					230				235					240	
Cys	Glu	Asp	Gly	Pro	Val	Phe	Tyr	Pro	Pro	Pro	Lys	Lys	Thr	Lys	
					245				250					255	
His															

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: LUNGTUT11
(B) CLONE: 2746976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60 :

Met Gln Phe Met Leu Leu Phe Ser Arg Gln Gly Lys Leu Arg Leu
5 10 15
Gln Lys Trp Tyr Val Pro Leu Ser Asp Lys Glu Lys Arg Lys Ile
20 25 30
Thr Arg Glu Leu Val Gln Thr Val Leu Ala Arg Lys Pro Lys Met
35 40 45
Cys Ser Phe Leu Glu Trp Arg Asp Leu Lys Ile Val Tyr Lys Arg
50 55 60
Tyr Ala Ser Leu Tyr Phe Cys Cys Ala Ile Glu Asp Gln Asp Asn
65 70 75
Glu Leu Ile Thr Leu Glu Ile Ile His Arg Tyr Val Glu Leu Leu
80 85 90
Asp Lys Tyr Phe Gly Ser Val Cys Glu Leu Asp Ile Ile Phe Asn
95 100 105
Phe Glu Lys Ala Tyr Phe Ile Leu Asp Glu Phe Leu Leu Gly Gly
110 115 120
Glu Val Gln Glu Thr Ser Lys Lys Asn Val Leu Lys Ala Ile Glu
125 130 135
Gln Ala Asp Leu Leu Gln Glu Asp Ala Lys Glu Ala Glu Thr Pro
140 145 150
Arg Ser Val Leu Glu Glu Ile Gly Leu Thr
155 160

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 341 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: THP1AZS08
(B) CLONE: 2753496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61 :

Met Lys Arg Ala Leu Gly Arg Arg Lys Gly Val Trp Leu Arg Leu
5 10 15
Arg Lys Ile Leu Phe Cys Val Leu Gly Leu Tyr Ile Ala Ile Pro
20 25 30
Phe Leu Ile Lys Leu Cys Pro Gly Ile Gln Ala Lys Leu Ile Phe
35 40 45
Leu Asn Phe Val Arg Val Pro Tyr Phe Ile Asp Leu Lys Lys Pro
50 55 60
Gln Asp Gln Gly Leu Asn His Thr Cys Asn Tyr Tyr Leu Gln Pro
65 70 75
Glu Glu Asp Val Thr Ile Gly Val Trp His Thr Val Pro Ala Val

80	85	90
Trp Trp Lys Asn Ala Gln Gly Lys Asp	Gln Met Trp Tyr Glu Asp	
95	100	105
Ala Leu Ala Ser Ser His Pro Ile Ile	Leu Tyr Leu His Gly Asn	
110	115	120
Ala Gly Thr Arg Gly Gly Asp His Arg	Val Glu Leu Tyr Lys Val	
125	130	135
Leu Ser Ser Leu Gly Tyr His Val Val	Thr Phe Asp Tyr Arg Gly	
140	145	150
Trp Gly Asp Ser Val Gly Thr Pro Ser	Glu Arg Gly Met Thr Tyr	
155	160	165
Asp Ala Leu His Val Phe Asp Trp Ile	Lys Ala Arg Ser Gly Asp	
170	175	180
Asn Pro Val Tyr Ile Trp Gly His Ser	Leu Gly Thr Gly Val Ala	
185	190	195
Thr Asn Leu Val Arg Arg Leu Cys Glu	Arg Glu Thr Pro Pro Asp	
200	205	210
Ala Leu Ile Leu Glu Ser Pro Phe Thr	Asn Ile Arg Glu Glu Ala	
215	220	225
Lys Ser His Pro Phe Ser Val Ile Tyr	Arg Tyr Phe Pro Gly Phe	
230	235	240
Asp Trp Phe Phe Leu Asp Pro Ile Thr	Ser Ser Gly Ile Lys Phe	
245	250	255
Ala Asn Asp Glu Asn Val Lys His Ile	Ser Cys Pro Leu Leu Ile	
260	265	270
Leu His Ala Glu Asp Asp Pro Val Val	Pro Phe Gln Leu Gly Arg	
275	280	285
Lys Leu Tyr Ser Ile Ala Ala Pro Ala	Arg Ser Phe Arg Asp Phe	
290	295	300
Lys Val Gln Phe Val Pro Phe His Ser	Asp Leu Gly Tyr Arg His	
305	310	315
Lys Tyr Ile Tyr Lys Ser Pro Glu Leu	Pro Arg Ile Leu Arg Glu	
320	325	330
Phe Leu Gly Lys Ser Glu Pro Glu His	Gln His	
335	340	

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARTUT03
- (B) CLONE: 2781553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62 :

Met Ala Glu Gly Glu Asp Val Gly Trp Trp Arg Ser Trp Leu Gln		
5	10	15
Gln Ser Tyr Gln Ala Val Lys Glu Lys Ser Ser Glu Ala Leu Glu		
20	25	30
Phe Met Lys Arg Asp Leu Thr Glu Phe Thr Gln Val Val Gln His		
35	40	45
Asp Thr Ala Cys Thr Ile Ala Ala Thr Ala Ser Val Val Lys Glu		
50	55	60

Lys Leu Ala Thr Glu Gly Ser Ser Gly Ala Thr Glu Lys Met Lys
 65 70 75
 Lys Gly Leu Ser Asp Phe Leu Gly Val Ile Ser Asp Thr Phe Ala
 80 85 90
 Pro Ser Pro Asp Lys Thr Ile Asp Cys Asp Val Ile Thr Leu Met
 95 100 105
 Gly Thr Pro Ser Gly Thr Ala Glu Pro Tyr Asp Gly Thr Lys Ala
 110 115 120
 Arg Leu Tyr Ser Leu Gln Ser Asp Pro Ala Thr Tyr Cys Asn Glu
 125 130 135
 Pro Asp Gly Pro Pro Glu Leu Phe Asp Ala Trp Leu Ser Gln Phe
 140 145 150
 Cys Leu Glu Glu Lys Lys Gly Glu Ile Ser Glu Leu Leu Val Gly
 155 160 165
 Ser Pro Ser Ile Arg Ala Leu Tyr Thr Lys Met Val Pro Ala Ala
 170 175 180
 Val Ser His Ser Glu Phe Trp His Arg Tyr Phe Tyr Lys Val His
 185 190 195
 Gln Leu Glu Gln Glu Gln Ala Arg Arg Asp Ala Leu Lys Gln Arg
 200 205 210
 Ala Glu Gln Ser Ile Ser Glu Glu Pro Gly Trp Glu Glu Glu
 215 220 225
 Glu Glu Leu Met Gly Ile Ser Pro Ile Ser Pro Lys Glu Ala Lys
 230 235 240
 Val Pro Val Ala Lys Ile Ser Thr Phe Pro Glu Gly Glu Pro Gly
 245 250 255
 Pro Gln Ser Pro Cys Glu Glu Asn Leu Val Thr Ser Val Glu Pro
 260 265 270
 Pro Ala Glu Val Thr Pro Ser Glu Ser Ser Glu Ser Ile Ser Leu
 275 280 285
 Val Thr Gln Ile Ala Asn Pro Ala Thr Ala Pro Glu Ala Arg Val
 290 295 300
 Leu Pro Lys Asp Leu Ser Gln Lys Leu Leu Glu Ala Ser Leu Glu
 305 310 315
 Glu Gln Gly Leu Ala Val Asp Val Gly Glu Thr Gly Pro Ser Pro
 320 325 330
 Pro Ile His Ser Lys Pro Leu Thr Pro Ala Gly His Thr Gly Gly
 335 340 345
 Pro Glu Pro Arg Pro Pro Ala Arg Val Glu Thr Leu Arg Glu Glu
 350 355 360
 Ala Pro Thr Asp Leu Arg Val Phe Glu Leu Asn Ser Asp Ser Gly
 365 370 375
 Lys Ser Thr Pro Ser Asn Asn Gly Lys Lys Gly Ser Ser Thr Asp
 380 385 390
 Ile Ser Glu Asp Trp Glu Lys Asp Phe Asp Leu Asp Met Thr Glu
 395 400 405
 Glu Glu Val Gln Met Ala Leu Ser Lys Val Asp Ala Ser Gly Glu
 410 415 420
 Leu Glu Asp Val Glu Trp Glu Asp Trp Glu
 425 430

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 143 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: ADRETUT06
(B) CLONE: 2821925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63 :

Met Gly Pro Val Arg Leu Gly Ile Leu Leu Phe Leu Phe Leu Ala
5 10 15
Val His Glu Ala Trp Ala Gly Met Leu Lys Glu Glu Asp Asp Asp
20 25 30
Thr Glu Arg Leu Pro Ser Lys Cys Glu Val Cys Lys Leu Leu Ser
35 40 45
Thr Glu Leu Gln Ala Glu Leu Ser Arg Thr Gly Arg Ser Arg Glu
50 55 60
Val Leu Glu Leu Gly Gln Val Leu Asp Thr Gly Lys Arg Lys Arg
65 70 75
His Val Pro Tyr Ser Val Ser Glu Thr Arg Leu Glu Glu Ala Leu
80 85 90
Glu Asn Leu Cys Glu Arg Ile Leu Asp Tyr Ser Val His Ala Glu
95 100 105
Arg Lys Gly Ser Leu Arg Tyr Ala Lys Gly Gln Ser Gln Thr Met
110 115 120
Ala Thr Leu Lys Gly Leu Val Gln Lys Gly Val Lys Val Asp Leu
125 130 135
Gly Ile Pro Leu Glu Leu Leu Gly
140

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: UTRSTUT05
(B) CLONE: 2879068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64 :

Met Glu Asp Met Asn Glu Tyr Ser Asn Ile Glu Glu Phe Ala Glu
5 10 15
Gly Ser Lys Ile Asn Ala Ser Lys Asn Gln Gln Asp Asp Gly Lys
20 25 30
Met Phe Ile Gly Gly Leu Ser Trp Asp Thr Ser Lys Lys Asp Leu
35 40 45
Thr Glu Tyr Leu Ser Arg Phe Gly Glu Val Val Asp Cys Thr Ile
50 55 60
Lys Thr Asp Pro Val Thr Gly Arg Ser Arg Gly Phe Gly Phe Val
65 70 75
Leu Phe Lys Asp Ala Ala Ser Val Asp Lys Val Leu Glu Leu Lys
80 85 90
Glu His Lys Leu Asp Gly Lys Leu Ile Asp Pro Lys Arg Ala Lys
95 100 105
Ala Leu Lys Gly Lys Glu Pro Pro Lys Lys Val Phe Val Gly Gly
110 115 120
Leu Ser Pro Asp Thr Ser Glu Glu Gln Ile Lys Glu Tyr Phe Gly

125		130		135										
Ala	Phe	Gly	Glu	Ile	Glu	Asn	Ile	Glu	Leu	Pro	Met	Asp	Thr	Lys
140										145				150
Thr	Asn	Glu	Arg	Arg	Gly	Phe	Cys	Phe	Ile	Thr	Tyr	Thr	Asp	Glu
155										160				165
Glu	Pro	Val	Lys	Lys	Leu	Leu	Glu	Ser	Arg	Tyr	His	Gln	Ile	Gly
170										175				180
Ser	Gly	Lys	Cys	Glu	Ile	Lys	Val	Ala	Gln	Pro	Lys	Glu	Val	Tyr
185										190				195
Arg	Gln	Gln	Gln	Gln	Gln	Gln	Lys	Gly	Gly	Arg	Gly	Ala	Ala	Ala
200										205				210
Gly	Gly	Arg	Gly	Gly	Thr	Arg	Gly	Arg	Gly	Arg	Gly	Gln	Gly	Gln
215										220				225
Asn	Trp	Asn	Gln	Gly	Phe	Asn	Asn	Tyr	Tyr	Asp	Gln	Gly	Tyr	Gly
230										235				240
Asn	Tyr	Asn	Ser	Ala	Tyr	Gly	Gly	Asp	Gln	Asn	Tyr	Ser	Gly	Tyr
245										250				255
Gly	Gly	Tyr	Asp	Tyr	Thr	Gly	Tyr	Asn	Tyr	Gly	Asn	Tyr	Gly	Tyr
260										265				270
Gly	Gln	Gly	Tyr	Ala	Asp	Tyr	Ser	Gly	Gln	Gln	Ser	Thr	Tyr	Gly
275										280				285
Lys	Ala	Ser	Arg	Gly	Gly	Gly	Asn	His	Gln	Asn	Asn	Tyr	Gln	Pro
290										295				300

Tyr

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SINJNOT02
- (B) CLONE: 2886757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65 :

Met	Gly	Glu	Pro	Gln	Gln	Val	Ser	Ala	Leu	Pro	Pro	Pro	Pro	Met
5									10					15
Gln	Tyr	Ile	Lys	Glu	Tyr	Thr	Asp	Glu	Asn	Ile	Gln	Glu	Gly	Leu
20										25				30
Ala	Pro	Lys	Pro	Pro	Pro	Ile	Lys	Asp	Ser	Tyr	Met	Met	Phe	
35										40				45
Gly	Asn	Gln	Phe	Gln	Cys	Asp	Asp	Leu	Ile	Ile	Arg	Pro	Leu	Glu
50										55				60
Ser	Gln	Gly	Ile	Glu	Arg	Leu	His	Pro	Met	Gln	Phe	Asp	His	Lys
65										70				75
Lys	Glu	Leu	Arg	Lys	Leu	Asn	Met	Ser	Ile	Leu	Ile	Asn	Phe	Leu
80										85				90
Asp	Leu	Leu	Asp	Ile	Leu	Ile	Arg	Ser	Pro	Gly	Ser	Ile	Lys	Arg
95										100				105
Glu	Glu	Lys	Leu	Glu	Asp	Leu	Lys	Leu	Leu	Phe	Val	His	Val	His
110										115				120
His	Leu	Ile	Asn	Glu	Tyr	Arg	Pro	His	Gln	Ala	Arg	Glu	Thr	Leu
125										130				135
Arg	Val	Met	Met	Glu	Val	Gln	Lys	Arg	Gln	Arg	Leu	Glu	Thr	Ala
140										145				150

Glu	Arg	Phe	Gln	Lys	His	Leu	Glu	Arg	Val	Ile	Glu	Met	Ile	Gln
				155					160					165
Asn	Cys	Leu	Ala	Ser	Leu	Pro	Asp	Asp	Leu	Pro	His	Ser	Glu	Ala
				170					175					180
Gly	Met	Arg	Val	Lys	Thr	Glu	Pro	Met	Asp	Ala	Asp	Asp	Ser	Asn
				185					190					195
Asn	Cys	Thr	Gly	Gln	Asn	Glu	His	Gln	Arg	Glu	Asn	Ser	Gly	His
				200					205					210
Arg	Arg	Asp	Gln	Ile	Ile	Glu	Lys	Asp	Ala	Ala	Leu	Cys	Val	Leu
				215					220					225
Ile	Asp	Glu	Met	Asn	Glu	Arg	Pro							
				230										

(2) INFORMATION FOR SEQ ID NO: 66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 354 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: SCORNTO4
 - (B) CLONE: 2964329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66 :

Met	Ala	Gly	Ala	Gly	Ala	Gly	Ala	Arg	Gly	Gly	Ala	Ala		
					5				10				15	
Ala	Gly	Val	Glu	Ala	Arg	Ala	Arg	Asp	Pro	Pro	Pro	Ala	His	Arg
					20				25				30	
Ala	His	Pro	Arg	His	Pro	Arg	Pro	Ala	Ala	Gln	Pro	Ser	Ala	Arg
					35					40			45	
Arg	Met	Asp	Gly	Gly	Ser	Gly	Gly	Leu	Gly	Ser	Gly	Asp	Asn	Ala
					50				55				60	
Pro	Thr	Thr	Glu	Ala	Leu	Phe	Val	Ala	Leu	Gly	Ala	Gly	Val	Thr
					65				70				75	
Ala	Leu	Ser	His	Pro	Leu	Leu	Tyr	Val	Lys	Leu	Leu	Ile	Gln	Val
					80				85				90	
Gly	His	Glu	Pro	Met	Pro	Pro	Thr	Leu	Gly	Thr	Asn	Val	Leu	Gly
					95				100				105	
Arg	Lys	Val	Leu	Tyr	Leu	Pro	Ser	Phe	Phe	Thr	Tyr	Ala	Lys	Tyr
					110				115				120	
Ile	Val	Gln	Val	Asp	Gly	Lys	Ile	Gly	Leu	Phe	Arg	Gly	Leu	Ser
					125				130				135	
Pro	Arg	Leu	Met	Ser	Asn	Ala	Leu	Ser	Thr	Val	Thr	Arg	Gly	Ser
					140				145				150	
Met	Lys	Lys	Val	Phe	Pro	Pro	Asp	Glu	Ile	Glu	Gln	Val	Ser	Asn
					155				160				165	
Lys	Asp	Asp	Met	Lys	Thr	Ser	Leu	Lys	Lys	Val	Val	Lys	Glu	Thr
					170				175				180	
Ser	Tyr	Glu	Met	Met	Met	Gln	Cys	Val	Ser	Arg	Met	Leu	Ala	His
					185				190				195	
Pro	Leu	His	Val	Ile	Ser	Met	Arg	Cys	Met	Val	Gln	Phe	Val	Gly
					200				205				210	
Arg	Glu	Ala	Lys	Tyr	Ser	Gly	Val	Leu	Ser	Ser	Ile	Gly	Lys	Ile
					215				220				225	
Phe	Lys	Glu	Glu	Gly	Leu	Leu	Gly	Phe	Phe	Val	Gly	Leu	Ile	Pro

	230	235	240											
His	Leu	Leu	Gly	Asp	Val	Val	Phe	Leu	Trp	Gly	Cys	Asn	Leu	Leu
	245	250	255											
Ala	His	Phe	Ile	Asn	Ala	Tyr	Leu	Val	Asp	Asp	Ser	Phe	Ser	Gln
	260	265	270											
Ala	Leu	Ala	Ile	Arg	Ser	Tyr	Thr	Lys	Phe	Val	Met	Gly	Ile	Ala
	275	280	285											
Val	Ser	Met	Leu	Thr	Tyr	Pro	Phe	Leu	Leu	Val	Gly	Asp	Leu	Met
	290	295	300											
Ala	Val	Asn	Asn	Cys	Gly	Leu	Gln	Ala	Gly	Leu	Pro	Pro	Tyr	Ser
	305	310	315											
Pro	Val	Phe	Lys	Ser	Trp	Ile	His	Cys	Trp	Lys	Tyr	Leu	Ser	Val
	320	325	330											
Gln	Gly	Gln	Leu	Phe	Arg	Gly	Ser	Ser	Leu	Leu	Phe	Arg	Arg	Val
	335	340	345											
Ser	Ser	Gly	Ser	Cys	Phe	Ala	Leu	Glu						
	350													

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SCORN0T04
- (B) CLONE: 2965248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67 :

Met	Ala	Ser	Thr	Ile	Ser	Ala	Tyr	Lys	Glu	Lys	Met	Lys	Glu	Leu
				5					10					15
Ser	Val	Leu	Ser	Leu	Ile	Cys	Ser	Cys	Phe	Tyr	Thr	Gln	Pro	His
				20					25					30
Pro	Asn	Thr	Val	Tyr	Gln	Tyr	Gly	Asp	Met	Glu	Val	Lys	Gln	Leu
				35					40					45
Asp	Lys	Arg	Ala	Ser	Gly	Gln	Ser	Phe	Glu	Val	Ile	Leu	Lys	Ser
				50					55					60
Pro	Ser	Asp	Leu	Ser	Pro	Glu	Ser	Pro	Met	Leu	Ser	Ser	Pro	Pro
				65					70					75
Lys	Lys	Lys	Asp	Thr	Ser	Leu	Glu	Glu	Leu	Gln	Lys	Arg	Leu	Glu
				80					85					90
Ala	Ala	Glu	Glu	Arg	Arg	Lys	Thr	Gln	Glu	Ala	Gln	Val	Leu	Lys
				95					100					105
Gln	Leu	Ala	Asp	Gly	Ala	Ser	Thr	Ser	Ala	Arg	Cys	Cys	Thr	Arg
				110					115					120
Arg	Trp	Arg	Arg	Ile	Thr	Thr	Ser	Ala	Ala	Arg	Arg	Arg	Arg	Ser
				125					130					135
Ser	Thr	Thr	Arg	Trp	Ser	Ser	Ala	Arg	Arg	Ser	Ala	Arg	His	Thr
				140					145					150
Trp	Pro	His	Cys	Ala	Ser	Gly	Cys	Ala	Arg	Arg	Ser	Cys	Thr	Arg
				155					160					165
Pro	Arg	Cys	Ala	Gly	Thr	Arg	Ser	Ser	Glu	Lys	Arg	Cys	Arg	Ala
				170					175					180
Lys	Gly	Pro	Gly	Arg	Ala	Ala	Pro	Ile	Leu	Arg	Arg	Asn	Thr	Phe
				185					190					195

Gly	Phe	Trp	Phe	Cys	Phe	Val	His	Leu	Cys	Leu	Asp	Ala	Thr	Phe
200									205					210
Val	Pro	Pro	Pro	Pro	Pro	Gln	Pro	Pro	Ala	Ser	Cys	Phe	Ser	Ser
									215		220			225
Ala	Leu	Ser	Arg	Pro	Ala	Leu	Ser	Ser	Trp					
									230		235			

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TLYMNOT06
- (B) CLONE: 3000534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68 :

Met	Trp	Ser	Ala	Gly	Arg	Gly	Gly	Ala	Ala	Trp	Pro	Val	Leu	Leu
5								10						15
Gly	Leu	Leu	Leu	Ala	Leu	Leu	Val	Pro	Gly	Gly	Gly	Ala	Ala	Lys
								20		25				30
Thr	Gly	Ala	Glu	Leu	Val	Thr	Cys	Gly	Ser	Val	Leu	Lys	Leu	Leu
								35		40				45
Asn	Thr	His	His	Arg	Val	Arg	Leu	His	Ser	His	Asp	Ile	Lys	Tyr
								50		55				60
Gly	Ser	Gly	Ser	Gly	Gln	Gln	Ser	Val	Thr	Gly	Val	Glu	Ala	Ser
					65			70						75
Asp	Asp	Ala	Asn	Ser	Tyr	Trp	Arg	Ile	Arg	Gly	Gly	Ser	Glu	Gly
					80			85						90
Gly	Cys	Pro	Arg	Gly	Ser	Pro	Val	Arg	Cys	Gly	Gln	Ala	Val	Arg
					95			100						105
Leu	Thr	His	Val	Leu	Thr	Gly	Lys	Asn	Leu	His	Thr	His	His	Phe
					110				115					120
Pro	Ser	Pro	Leu	Ser	Asn	Asn	Gln	Glu	Val	Ser	Ala	Phe	Gly	Glu
					125				130					135
Asp	Gly	Glu	Gly	Asp	Asp	Leu	Asp	Leu	Trp	Thr	Val	Arg	Cys	Ser
					140				145					150
Gly	Gln	His	Trp	Glu	Arg	Glu	Ala	Ala	Val	Arg	Phe	Gln	His	Val
					155				160					165
Gly	Thr	Ser	Val	Phe	Leu	Ser	Val	Thr	Gly	Glu	Gln	Tyr	Gly	Ser
					170				175					180
Pro	Ile	Arg	Gly	Gln	His	Glu	Val	His	Gly	Met	Pro	Ser	Ala	Asn
					185				190					195
Thr	His	Asn	Thr	Trp	Lys	Ala	Met	Glu	Gly	Ile	Phe	Ile	Lys	Pro
					200				205					210
Ser	Val	Glu	Pro	Ser	Ala	Gly	His	Asp	Glu	Leu				
					215				220					

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: HEAANOT01
 - (B) CLONE: 3046870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69 :

Met	Lys	Ala	Phe	His	Thr	Phe	Cys	Val	Val	Leu	Leu	Val	Phe	Gly
					5				10					15
Ser	Val	Ser	Glu	Ala	Lys	Phe	Asp	Asp	Phe	Glu	Asp	Glu	Glu	Asp
						20			25					30
Ile	Val	Glu	Tyr	Asp	Asp	Asn	Asp	Phe	Ala	Glu	Phe	Glu	Asp	Val
						35			40					45
Met	Glu	Asp	Ser	Val	Thr	Glu	Ser	Pro	Gln	Arg	Val	Ile	Ile	Thr
					50				55					60
Glu	Asp	Asp	Glu	Asp	Glu	Thr	Thr	Val	Glu	Leu	Glu	Gly	Gln	Asp
					65				70					75
Glu	Asn	Gln	Glu	Gly	Asp	Phe	Glu	Asp	Ala	Asp	Thr	Gln	Glu	Gly
					80				85					90
Asp	Thr	Glu	Ser	Glu	Pro	Tyr	Asp	Asp	Glu	Glu	Phe	Glu	Gly	Tyr
					95				100					105
Glu	Asp	Lys	Pro	Asp	Thr	Ser	Ser	Ser	Lys	Asn	Lys	Asp	Pro	Ile
					110				115					120
Thr	Ile	Val	Asp	Val	Pro	Ala	His	Leu	Gln	Asn	Ser	Trp	Glu	Ser
					125				130					135
Tyr	Tyr	Leu	Glu	Ile	Leu	Met	Val	Thr	Gly	Leu	Leu	Ala	Tyr	Ile
					140				145					150
Met	Asn	Tyr	Ile	Ile	Gly	Lys	Asn	Lys	Asn	Ser	Arg	Leu	Ala	Gln
					155				160					165
Ala	Trp	Phe	Asn	Thr	His	Arg	Glu	Leu	Leu	Glu	Ser	Asn	Phe	Thr
					170				175					180
Leu	Val	Gly	Asp	Asp	Gly	Thr	Asn	Lys	Glu	Ala	Thr	Ser	Thr	Gly
					185				190					195
Lys	Leu	Asn	Gln	Glu	Asn	Glu	His	Ile	Tyr	Asn	Leu	Trp	Cys	Ser
					200				205					210
Gly	Arg	Val	Cys	Cys	Glu	Gly	Met	Leu	Ile	Gln	Leu	Arg	Phe	Leu
					215				220					225
Lys	Arg	Gln	Asp	Leu	Leu	Asn	Val	Leu	Ala	Arg	Met	Met	Arg	Pro
					230				235					240
Val	Ser	Asp	Gln	Val	Gln	Ile	Lys	Val	Thr	Met	Asn	Asp	Glu	Asp
					245				250					255
Met	Asp	Thr	Tyr	Val	Phe	Ala	Val	Gly	Thr	Arg	Lys	Ala	Leu	Val
					260				265					270
Arg	Leu	Gln	Lys	Glu	Met	Gln	Asp	Leu	Ser	Glu	Phe	Cys	Ser	Asp
					275				280					285
Lys	Pro	Lys	Ser	Gly	Ala	Lys	Tyr	Gly	Leu	Pro	Asp	Ser	Leu	Ala
					290				295					300
Ile	Leu	Ser	Glu	Met	Gly	Glu	Val	Thr	Asp	Gly	Met	Met	Asp	Thr
					305				310					315
Lys	Met	Val	His	Phe	Leu	Thr	His	Tyr	Ala	Asp	Lys	Ile	Glu	Ser
					320				325					330
Val	His	Phe	Ser	Asp	Gln	Phe	Ser	Gly	Pro	Lys	Ile	Met	Gln	Glu
					335				340					345
Glu	Gly	Gln	Pro	Leu	Lys	Leu	Pro	Asp	Thr	Lys	Arg	Thr	Leu	Leu
					350				355					360
Phe	Thr	Phe	Asn	Val	Pro	Gly	Ser	Gly	Asn	Thr	Tyr	Pro	Lys	Asp
					365				370					375

Met	Glu	Ala	Leu	Leu	Pro	Leu	Met	Asn	Met	Val	Ile	Tyr	Ser	Ile
					380				385					390
Asp	Lys	Ala	Lys	Lys	Phe	Arg	Leu	Asn	Arg	Glu	Gly	Lys	Gln	Lys
					395				400					405
Ala	Asp	Lys	Asn	Arg	Ala	Arg	Val	Glu	Glu	Asn	Phe	Leu	Lys	Leu
					410				415					420
Thr	His	Val	Gln	Arg	Gln	Glu	Ala	Ala	Gln	Ser	Arg	Arg	Glu	Glu
					425				430					435
Lys	Lys	Arg	Ala	Glu	Lys	Glu	Arg	Ile	Met	Asn	Glu	Glu	Asp	Pro
					440				445					450
Glu	Lys	Gln	Arg	Arg	Leu	Glu	Glu	Ala	Ala	Leu	Arg	Arg	Glu	Gln
					455				460					465
Lys	Lys	Leu	Glu	Lys	Lys	Gln	Met	Lys	Met	Lys	Gln	Ile	Lys	Val
					470				475					480
Lys	Ala	Met												

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PONSAZT01
- (B) CLONE: 3057669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70 :

Met	Asp	His	Glu	Asp	Ile	Ser	Glu	Ser	Val	Asp	Ala	Ala	Tyr	Asn
					5				10					15
Leu	Gln	Asp	Ser	Cys	Leu	Thr	Asp	Cys	Asp	Val	Glu	Asp	Gly	Thr
						20				25				30
Met	Asp	Gly	Asn	Asp	Glu	Gly	His	Ser	Phe	Glu	Leu	Cys	Pro	Ser
							35			40				45
Glu	Ala	Ser	Pro	Tyr	Val	Arg	Ser	Arg	Glu	Arg	Thr	Ser	Ser	Ser
							50			55				60
Ile	Val	Phe	Glu	Asp	Ser	Gly	Cys	Asp	Asn	Ala	Ser	Ser	Lys	Glu
							65			70				75
Glu	Pro	Lys	Thr	Asn	Arg	Leu	His	Ile	Gly	Asn	His	Cys	Ala	Asn
							80			85				90
Lys	Leu	Thr	Ala	Phe	Lys	Pro	Thr	Ser	Ser	Lys	Ser	Ser	Ser	Glu
							95			100				105
Ala	Thr	Leu	Ser	Ile	Ser	Pro	Pro	Arg	Pro	Thr	Thr	Leu	Ser	Leu
							110			115				120
Asp	Leu	Thr	Lys	Asn	Thr	Thr	Glu	Lys	Leu	Gln	Pro	Ser	Ser	Pro
							125			130				135
Lys	Val	Tyr	Leu	Tyr	Ile	Gln	Met	Gln	Leu	Cys	Arg	Lys	Glu	Asn
							140			145				150
Leu	Lys	Asp	Trp	Met	Asn	Gly	Arg	Cys	Thr	Ile	Glu	Glu	Arg	Glu
							155			160				165
Arg	Ser	Val	Cys	Leu	His	Ile	Phe	Leu	Gln	Ile	Ala	Glu	Ala	Val
							170			175				180
Glu	Phe	Leu	His	Ser	Lys	Gly	Leu	Met	His	Arg	Asp	Leu	Lys	Pro
							185			190				195
Ser	Asn	Ile	Phe	Phe	Thr	Met	Asp	Asp	Val	Val	Lys	Val	Gly	Asp
							200			205				210
Phe	Gly	Leu	Val	Thr	Ala	Met	Asp	Gln	Asp	Glu	Glu	Gln	Thr	

215	220	225												
Val	Leu	Thr	Pro	Met	Pro	Ala	Tyr	Ala	Arg	His	Thr	Gly	Gln	Val
230	235	240												
Gly	Thr	Lys	Leu	Tyr	Met	Ser	Pro	Glu	Gln	Ile	His	Gly	Asn	Ser
245	250	255												
Tyr	Ser	His	Lys	Val	Asp	Ile	Phe	Ser	Leu	Gly	Leu	Ile	Leu	Phe
260	265	270												
Glu	Leu	Leu	Tyr	Pro	Phe	Ser	Thr	Gln	Met	Glu	Arg	Val	Arg	Thr
275	280	285												
Leu	Thr	Asp	Val	Arg	Asn	Leu	Lys	Phe	Pro	Pro	Leu	Phe	Thr	Gln
290	295	300												
Lys	Tyr	Pro	Cys	Glu	Tyr	Val	Met	Val	Gln	Asp	Met	Leu	Ser	Pro
305	310	315												
Ser	Pro	Met	Glu	Arg	Pro	Glu	Ala	Ile	Asn	Ile	Ile	Glu	Asn	Ala
320	325	330												
Val	Phe	Glu	Asp	Leu	Asp	Phe	Pro	Gly	Lys	Thr	Val	Leu	Arg	Gln
335	340	345												
Arg	Ser	Arg	Ser	Leu	Ser	Ser	Ser	Gly	Thr	Lys	His	Ser	Arg	Gln
350	355	360												
Ser	Asn	Asn	Ser	His	Ser	Pro	Leu	Pro	Ser	Asn				
365	370													

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: HEAONOT03
- (B) CLONE: 3088178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71 :

Met	Met	Asn	Asn	Arg	Phe	Arg	Lys	Asp	Met	Met	Lys	Asn	Ala	Ser
5									10					15
Glu	Ser	Lys	Leu	Ser	Lys	Asp	Asn	Leu	Lys	Lys	Arg	Leu	Lys	Glu
									20	25				30
Glu	Phe	Gln	His	Ala	Met	Gly	Gly	Val	Pro	Ala	Trp	Ala	Glu	Thr
									35	40				45
Thr	Lys	Arg	Lys	Thr	Ser	Ser	Asp	Asp	Glu	Ser	Glu	Glu	Asp	Glu
									50	55				60
Asp	Asp	Leu	Leu	Gln	Arg	Thr	Gly	Asn	Phe	Ile	Ser	Thr	Ser	Thr
									65	70				75
Ser	Leu	Pro	Arg	Gly	Ile	Leu	Lys	Met	Lys	Asn	Cys	Gln	His	Ala
									80	85				90
Asn	Ala	Glu	Arg	Pro	Thr	Val	Ala	Arg	Ile	Ser	Ser	Val	Gln	Phe
									95	100				105
His	Pro	Gly	Ala	Gln	Ile	Val	Met	Val	Ala	Gly	Leu	Asp	Asn	Ala
									110	115				120
Val	Ser	Leu	Phe	Gln	Val	Asp	Gly	Lys	Thr	Asn	Pro	Lys	Ile	Gln
									125	130				135
Ser	Ile	Tyr	Leu	Glu	Arg	Phe	Pro	Ile	Phe	Lys	Ala	Cys	Phe	Ser
									140	145				150
Ala	Asn	Gly	Glu	Glu	Val	Leu	Ala	Thr	Ser	Thr	His	Ser	Lys	Val
									155	160				165

Leu	Tyr	Val	Tyr	Asp	Met	Leu	Ala	Gly	Lys	Leu	Ile	Pro	Val	His
					170				175					180
Gln	Val	Arg	Gly	Leu	Lys	Glu	Lys	Ile	Val	Arg	Ser	Phe	Glu	Val
					185				190					195
Ser	Pro	Asp	Gly	Ser	Phe	Leu	Leu	Ile	Asn	Gly	Ile	Ala	Gly	Tyr
					200				205					210
Leu	His	Leu	Leu	Ala	Met	Lys	Thr	Lys	Glu	Leu	Ile	Gly	Ser	Met
					215				220					225
Lys	Ile	Asn	Gly	Arg	Val	Ala	Ala	Ser	Thr	Phe	Ser	Ser	Asp	Ser
					230				235					240
Lys	Lys	Val	Tyr	Ala	Ser	Ser	Gly	Asp	Gly	Glu	Val	Tyr	Val	Trp
					245				250					255
Asp	Val	Asn	Ser	Arg	Lys	Cys	Leu	Asn	Arg	Phe	Val	Asp	Glu	Gly
					260				265					270
Ser	Leu	Tyr	Gly	Leu	Ser	Ile	Ala	Thr	Ser	Arg	Asn	Gly	Gln	Tyr
					275				280					285
Val	Ala	Cys	Gly	Ser	Asn	Cys	Gly	Val	Val	Asn	Ile	Tyr	Asn	Gln
					290				295					300
Asp	Ser	Cys	Leu	Gln	Glu	Thr	Asn	Pro	Lys	Pro	Ile	Lys	Ala	Ile
					305				310					315
Met	Asn	Leu	Val	Thr	Gly	Val	Thr	Ser	Leu	Thr	Phe	Asn	Pro	Thr
					320				325					330
Thr	Glu	Ile	Leu	Ala	Ile	Ala	Ser	Glu	Lys	Met	Lys	Glu	Ala	Val
					335				340					345
Arg	Leu	Val	His	Leu	Pro	Ser	Cys	Thr	Val	Phe	Ser	Asn	Phe	Pro
					350				355					360
Val	Ile	Lys	Asn	Lys	Asn	Ile	Ser	His	Val	His	Thr	Met	Asp	Phe
					365				370					375
Ser	Pro	Arg	Ser	Gly	Tyr	Phe	Ala	Leu	Gly	Asn	Glu	Lys	Gly	Lys
					380				385					390
Ala	Leu	Met	Tyr	Arg	Leu	His	His	Tyr	Ser	Asp	Phe			
					395				400					

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT19
- (B) CLONE: 3094321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72 :

Met	Ala	Leu	Ser	Arg	Gly	Leu	Pro	Arg	Glu	Leu	Ala	Glu	Ala	Val
					5				10					15
Ala	Gly	Gly	Arg	Val	Leu	Val	Val	Gly	Ala	Gly	Gly	Ile	Gly	Cys
					20				25					30
Glu	Leu	Leu	Lys	Asn	Leu	Val	Leu	Thr	Gly	Phe	Ser	His	Ile	Asp
					35				40					45
Leu	Ile	Asp	Leu	Asp	Thr	Ile	Asp	Val	Ser	Asn	Leu	Asn	Arg	Gln
					50				55					60
Phe	Leu	Phe	Gln	Lys	Lys	His	Val	Gly	Arg	Ser	Lys	Ala	Gln	Val
					65				70					75
Ala	Lys	Glu	Ser	Val	Leu	Gln	Phe	Tyr	Pro	Lys	Ala	Asn	Ile	Val

80	85	90												
Ala	Tyr	His	Asp	Ser	Ile	Met	Asn	Pro	Asp	Tyr	Asn	Val	Glu	Phe
95										100				105
Phe	Arg	Gln	Phe	Ile	Leu	Val	Met	Asn	Ala	Leu	Asp	Asn	Arg	Ala
110										115				120
Ala	Arg	Asn	His	Val	Asn	Arg	Met	Cys	Leu	Ala	Ala	Asp	Val	Pro
125										130				135
Leu	Ile	Glu	Ser	Gly	Thr	Ala	Gly	Tyr	Leu	Gly	Gln	Val	Thr	Thr
140										145				150
Ile	Lys	Lys	Gly	Val	Thr	Glu	Cys	Tyr	Glu	Cys	His	Pro	Lys	Pro
155										160				165
Thr	Gln	Arg	Thr	Phe	Pro	Gly	Cys	Thr	Ile	Arg	Asn	Thr	Pro	Ser
170										175				180
Glu	Pro	Ile	His	Cys	Ile	Val	Trp	Ala	Lys	Tyr	Leu	Phe	Asn	Gln
185										190				195
Leu	Phe	Gly	Glu	Glu	Asp	Ala	Asp	Gln	Glu	Val	Ser	Pro	Asp	Arg
200										205				210
Ala	Asp	Pro	Glu	Ala	Ala	Trp	Glu	Pro	Thr	Glu	Ala	Glu	Ala	Arg
215										220				225
Ala	Arg	Ala	Ser	Asn	Glu	Asp	Gly	Asp	Ile	Lys	Arg	Ile	Ser	Thr
230										235				240
Lys	Glu	Trp	Ala	Lys	Ser	Thr	Gly	Tyr	Asp	Pro	Val	Lys	Leu	Phe
245										250				255
Thr	Lys	Leu	Phe	Lys	Asp	Asp	Ile	Arg	Tyr	Leu	Leu	Thr	Met	Asp
260										265				270
Lys	Leu	Trp	Arg	Lys	Arg	Lys	Pro	Pro	Val	Pro	Leu	Asp	Trp	Ala
275										280				285
Glu	Val	Gln	Ser	Gln	Gly	Glu	Glu	Thr	Asn	Ala	Ser	Asp	Gln	Gln
290										295				300
Asn	Glu	Pro	Gln	Leu	Gly	Leu	Lys	Asp	Gln	Gln	Val	Leu	Asp	Val
305										310				315
Lys	Ser	Tyr	Ala	Arg	Leu	Phe	Ser	Lys	Ser	Ile	Glu	Thr	Leu	Arg
320										325				330
Val	His	Leu	Ala	Glu	Lys	Gly	Asp	Gly	Ala	Glu	Leu	Ile	Trp	Asp
335										340				345
Lys	Asp	Asp	Pro	Ser	Ala	Met	Asp	Phe	Val	Thr	Ser	Ala	Ala	Asn
350										355				360
Leu	Arg	Met	His	Ile	Phe	Ser	Met	Asn	Met	Lys	Ser	Arg	Phe	Asp
365										370				375
Ile	Lys	Ser	Met	Ala	Gly	Asn	Ile	Ile	Pro	Ala	Ile	Ala	Thr	Thr
380										385				390
Asn	Ala	Val	Ile	Ala	Gly	Leu	Ile	Val	Leu	Glu	Gly	Leu	Lys	Ile
395										400				405
Leu	Ser	Gly	Lys	Ile	Asp	Gln	Cys	Arg	Thr	Ile	Phe	Leu	Asn	Lys
410										415				420
Gln	Pro	Asn	Pro	Arg	Lys	Lys	Leu	Leu	Val	Pro	Cys	Ala	Leu	Asp
425										430				435
Pro	Pro	Asn	Pro	Asn	Cys	Tyr	Val	Cys	Ala	Ser	Lys	Pro	Glu	Val
440										445				450
Thr	Val	Arg	Leu	Asn	Val	His	Lys	Val	Thr	Val	Leu	Thr	Leu	Gln
455										460				465
Asp	Lys	Ile	Val	Lys	Glu	Lys	Phe	Ala	Met	Val	Ala	Pro	Asp	Val
470										475				480
Gln	Ile	Glu	Asp	Gly	Lys	Gly	Thr	Ile	Leu	Ile	Ser	Ser	Glu	Glu
485										490				495
Gly	Glu	Thr	Glu	Ala	Asn	Asn	His	Lys	Lys	Leu	Ser	Glu	Phe	Gly
500										505				510
Ile	Arg	Asn	Gly	Ser	Arg	Leu	Gln	Ala	Asp	Asp	Phe	Leu	Gln	Asp
515										520				525
Tyr	Thr	Leu	Leu	Ile	Asn	Ile	Leu	His	Ser	Glu	Asp	Leu	Gly	Lys
530										535				540

Asp	Val	Glu	Phe	Glu	Val	Val	Gly	Asp	Ala	Pro	Glu	Lys	Val	Gly
				545					550				555	
Pro	Lys	Gln	Ala	Glu	Asp	Ala	Ala	Lys	Ser	Ile	Thr	Asn	Gly	Ser
				560					565				570	
Asp	Asp	Gly	Ala	Gln	Pro	Ser	Thr	Ser	Thr	Ala	Gln	Glu	Gln	Asp
				575					580				585	
Asp	Val	Leu	Ile	Val	Asp	Ser	Asp	Glu	Glu	Asp	Ser	Ser	Asn	Asn
				590					595				600	
Ala	Asp	Val	Ser	Glu	Glu	Glu	Arg	Ser	Arg	Lys	Arg	Lys	Leu	Asp
				605					610				615	
Glu	Lys	Glu	Asn	Leu	Ser	Ala	Lys	Arg	Ser	Arg	Ile	Glu	Gln	Lys
				620					625				630	
Glu	Glu	Leu	Asp	Asp	Val	Ile	Ala	Leu	Asp					
				635					640					

(2) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: LUNGTUT13
 - (B) CLONE: 3115936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73 :

Met	Asp	Lys	Ile	Leu	Asn	Val	Glu	Glu	Thr	Tyr	Leu	Thr	Val	Leu
				5					10				15	
Val	Lys	Ile	Gly	Pro	Gly	Phe	His	Thr	Arg	Glu	Cys	Phe	Leu	Leu
				20					25				30	
Lys	Ser	Ile	Leu	Cys	Phe	Ser	Pro	Ser	Tyr	Arg	Met	Ser	Glu	Gly
				35					40				45	
Asp	Ser	Val	Gly	Glu	Ser	Val	His	Gly	Lys	Pro	Ser	Val	Val	Tyr
				50					55				60	
Arg	Phe	Phe	Thr	Arg	Leu	Gly	Gln	Ile	Tyr	Gln	Ser	Trp	Leu	Asp
				65					70				75	
Lys	Ser	Thr	Pro	Tyr	Thr	Ala	Val	Arg	Trp	Val	Val	Thr	Leu	Gly
				80					85				90	
Leu	Ser	Phe	Val	Tyr	Met	Ile	Arg	Val	Tyr	Leu	Leu	Gln	Gly	Trp
				95					100				105	
Tyr	Ile	Val	Thr	Tyr	Ala	Leu	Gly	Ile	Tyr	His	Leu	Asn	Leu	Phe
				110					115				120	
Ile	Ala	Phe	Leu	Ser	Pro	Lys	Val	Asp	Pro	Ser	Leu	Met	Glu	Asp
				125					130				135	
Ser	Asp	Asp	Gly	Pro	Ser	Leu	Pro	Thr	Lys	Gln	Asn	Glu	Glu	Phe
				140					145				150	
Arg	Pro	Phe	Ile	Arg	Arg	Leu	Pro	Glu	Phe	Lys	Phe	Trp	His	Ala
				155					160				165	
Ala	Thr	Lys	Gly	Ile	Leu	Val	Ala	Met	Val	Cys	Thr	Phe	Phe	Asp
				170					175				180	
Ala	Phe	Asn	Val	Pro	Val	Phe	Trp	Pro	Ile	Leu	Val	Met	Tyr	Phe
				185					190				195	
Ile	Met	Leu	Phe	Cys	Ile	Thr	Met	Lys	Arg	Gln	Ile	Lys	His	Met
				200					205				210	
Ile	Lys	Tyr	Arg	Tyr	Ile	Pro	Phe	Thr	His	Gly	Lys	Arg	Arg	Tyr

215	220	225
Arg Gly Lys Glu Asp Ala Gly Lys Ala Phe Ala Ser		
230	235	

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT13
- (B) CLONE: 3116522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74 :

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro	15
5	10
Ser Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser	30
20	25
Trp Thr Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly	45
35	40
Tyr Ala Ser Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe	60
50	55
Arg Arg Lys Asn Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro	75
65	70
Leu Val Lys Ala Cys Val Phe Gly Asn Glu Pro Lys Ala Ser Asp	90
80	85
Glu Val Pro Leu Ala Pro Arg Thr Glu Ala Ala Glu Thr Thr Pro	105
95	100
Met Trp Gln Ala Leu Lys Leu Leu Phe Cys Ala Thr Gly Leu Gln	120
110	115
Val Ser Tyr Leu Thr Trp Gly Val Leu Gln Glu Arg Val Met Thr	135
125	130
Arg Ser Tyr Gly Ala Thr Ala Thr Ser Pro Gly Glu Arg Phe Thr	150
140	145
Asp Ser Gln Phe Leu Val Leu Met Asn Arg Val Leu Ala Leu Ile	165
155	160
Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln Pro Arg His Gly	180
170	175
Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser Asn Val Leu	195
185	190
Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser Phe Pro	210
200	205
Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met Leu	225
215	220
Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr	240
230	235
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu	255
245	250
Ser Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser	270
260	265
Gly Leu Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr	285
275	280
Ser Asn Trp Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val	300
290	295

Gln	Met	Met	Phe	Gly	Val	Asn	Phe	Phe	Ser	Cys	Leu	Phe	Thr	Val
			305						310					315
Gly	Ser	Leu	Leu	Glu	Gln	Gly	Ala	Leu	Leu	Glu	Gly	Thr	Arg	Phe
			320						325					330
Met	Gly	Arg	His	Ser	Glu	Phe	Ala	Ala	His	Ala	Leu	Leu	Leu	Ser
			335						340					345
Ile	Cys	Ser	Ala	Cys	Gly	Gln	Leu	Phe	Ile	Phe	Tyr	Thr	Ile	Gly
			350						355					360
Gln	Phe	Gly	Ala	Ala	Val	Phe	Thr	Ile	Ile	Met	Thr	Leu	Arg	Gln
			365						370					375
Ala	Phe	Ala	Ile	Leu	Leu	Ser	Cys	Leu	Leu	Tyr	Gly	His	Thr	Val
			380						385					390
Thr	Val	Val	Gly	Gly	Leu	Gly	Val	Ala	Val	Val	Phe	Ala	Ala	Leu
			395						400					405
Leu	Leu	Arg	Val	Tyr	Ala	Arg	Gly	Arg	Leu	Lys	Gln	Arg	Gly	Lys
			410						415					420
Lys	Ala	Val	Pro	Val	Glu	Ser	Pro	Val	Gln	Lys	Val			
			425						430					

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT13
- (B) CLONE: 3117184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75 :

Met	Ser	Phe	Pro	Pro	His	Leu	Asn	Arg	Pro	Pro	Met	Gly	Ile	Pro
					5				10					15
Ala	Leu	Pro	Pro	Gly	Thr	Pro	Pro	Pro	Gln	Phe	Pro	Gly	Phe	Pro
					20					25				30
Pro	Pro	Val	Pro	Pro	Gly	Thr	Pro	Met	Ile	Pro	Val	Pro	Met	Ser
					35				40					45
Ile	Met	Ala	Pro	Ala	Pro	Thr	Val	Leu	Val	Pro	Thr	Val	Ser	Met
					50				55					60
Val	Gly	Lys	His	Leu	Gly	Ala	Arg	Lys	Asp	His	Pro	Gly	Leu	Lys
					65				70					75
Ala	Lys	Glu	Asn	Asp	Glu	Asn	Cys	Gly	Pro	Thr	Thr	Thr	Val	Phe
					80				85					90
Val	Gly	Asn	Ile	Ser	Glu	Lys	Ala	Ser	Asp	Met	Leu	Ile	Arg	Gln
					95				100					105
Leu	Leu	Ala	Lys	Cys	Gly	Leu	Val	Leu	Ser	Trp	Lys	Arg	Val	Gln
					110				115					120
Gly	Ala	Ser	Gly	Lys	Leu	Gln	Ala	Phe	Gly	Phe	Cys	Glu	Tyr	Lys
					125				130					135
Glu	Pro	Glu	Ser	Thr	Leu	Arg	Ala	Leu	Arg	Leu	Leu	His	Asp	Leu
					140				145					150
Gln	Ile	Gly	Glu	Lys	Lys	Leu	Leu	Val	Lys	Val	Asp	Ala	Lys	Thr
					155				160					165
Lys	Ala	Gln	Leu	Asp	Glu	Trp	Lys	Ala	Lys	Lys	Lys	Ala	Ser	Asn
					170				175					180
Gly	Asn	Ala	Arg	Pro	Glu	Thr	Val	Thr	Asn	Asp	Asp	Glu	Glu	Ala

	185		190		195									
Leu	Asp	Glu	Glu	Thr	Lys	Arg	Arg	Asp	Gln	Met	Ile	Lys	Gly	Ala
				200					205					210
Ile	Glu	Val	Leu	Ile	Arg	Glu	Tyr	Ser	Ser	Glu	Leu	Asn	Ala	Pro
				215					220					225
Ser	Gln	Glu	Ser	Asp	Ser	His	Pro	Arg	Lys	Lys	Lys	Glu	Lys	
				230					235					240
Lys	Glu	Asp	Ile	Phe	Gly	Arg	Phe	Gln	Trp	Ala	His			
				245					250					

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LNODNOT05
- (B) CLONE: 3125156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76 :

Met	Gly	Pro	Gln	Ala	Ala	Pro	Leu	Thr	Ile	Arg	Gly	Pro	Ser	Ser
				5					10					15
Ala	Gly	Gln	Ser	Thr	Pro	Ser	Pro	His	Leu	Val	Pro	Ser	Pro	Ala
				20					25					30
Pro	Ser	Pro	Gly	Pro	Gly	Pro	Val	Pro	Pro	Arg	Pro	Pro	Ala	Ala
				35					40					45
Glu	Pro	Pro	Pro	Cys	Leu	Arg	Arg	Gly	Ala	Ala	Ala	Ala	Asp	Leu
				50					55					60
Leu	Ser	Ser	Ser	Pro	Glu	Ser	Gln	His	Gly	Gly	Thr	Gln	Ser	Pro
				65					70					75
Gly	Gly	Gly	Gln	Pro	Leu	Leu	Gln	Pro	Thr	Lys	Val	Asp	Ala	Ala
				80					85					90
Glu	Gly	Arg	Arg	Pro	Gln	Ala	Leu	Arg	Leu	Ile	Glu	Arg	Asp	Pro
				95					100					105
Tyr	Glu	His	Pro	Glu	Arg	Leu	Arg	Gln	Leu	Gln	Gln	Glu	Leu	Glu
				110					115					120
Ala	Phe	Arg	Gly	Gln	Leu	Gly	Asp	Val	Gly	Ala	Leu	Asp	Thr	Val
				125					130					135
Trp	Arg	Glu	Leu	Gln	Asp	Ala	Gln	Glu	His	Asp	Ala	Arg	Gly	Arg
				140					145					150
Ser	Ile	Ala	Ile	Ala	Arg	Cys	Tyr	Ser	Leu	Lys	Asn	Arg	His	Gln
				155					160					165
Asp	Val	Met	Pro	Tyr	Asp	Ser	Asn	Arg	Val	Val	Leu	Arg	Ser	Gly
				170					175					180
Lys	Asp	Asp	Tyr	Ile	Asn	Ala	Ser	Cys	Val	Glu	Gly	Leu	Ser	Pro
				185					190					195
Tyr	Cys	Pro	Pro	Leu	Val	Ala	Thr	Gln	Ala	Pro	Leu	Pro	Gly	Thr
				200					205					210
Ala	Ala	Asp	Phe	Trp	Leu	Met	Val	His	Glu	Gln	Lys	Val	Ser	Val
				215					220					225
Ile	Val	Met	Leu	Val	Ser	Glu	Ala	Glu	Met	Glu	Lys	Gln	Lys	Val
				230					235					240
Ala	Arg	Tyr	Phe	Pro	Thr	Glu	Arg	Gly	Gln	Pro	Met	Val	His	Gly
				245					250					255

Ala	Leu	Ser	Leu	Ala	Leu	Ser	Ser	Val	Arg	Ser	Thr	Glu	Thr	His
				260				265						270
Val	Glu	Arg	Val	Leu	Ser	Leu	Gln	Phe	Arg	Asp	Gln	Ser	Leu	Lys
				275				280						285
Arg	Ser	Leu	Val	His	Leu	His	Phe	Pro	Thr	Trp	Pro	Glu	Leu	Gly
				290				295						300
Leu	Pro	Asp	Ser	Pro	Ser	Asn	Leu	Leu	Arg	Phe	Ile	Gln	Glu	Val
				305				310						315
His	Ala	His	Tyr	Leu	His	Gln	Arg	Pro	Leu	His	Thr	Pro	Ile	Ile
				320				325						330
Val	His	Cys	Ser	Ser	Gly	Val	Gly	Arg	Thr	Gly	Ala	Phe	Ala	Leu
				335				340						345
Leu	Tyr	Ala	Ala	Val	Gln	Glu	Val	Glu	Ala	Gly	Asn	Gly	Ile	Pro
				350				355						360
Glu	Leu	Pro	Gln	Leu	Val	Arg	Arg	Met	Arg	Gln	Gln	Arg	Lys	His
				365				370						375
Met	Leu	Gln	Glu	Lys	Leu	His	Leu	Arg	Phe	Cys	Tyr	Glu	Ala	Val
				380				385						390
Val	Arg	His	Val	Glu	Gln	Val	Leu	Gln	Arg	His	Gly	Val	Pro	Pro
				395				400						405
Pro	Cys	Lys	Pro	Leu	Ala	Ser	Ala	Ser	Ile	Ser	Gln	Lys	Asn	His
				410				415						420
Leu	Pro	Gln	Asp	Ser	Gln	Asp	Leu	Val	Leu	Gly	Gly	Asp	Val	Pro
				425				430						435
Ile	Ser	Ser	Ile	Gln	Ala	Thr	Ile	Ala	Lys	Leu	Ser	Ile	Arg	Pro
				440				445						450
Pro	Gly	Gly	Leu	Glu	Ser	Pro	Val	Ala	Ser	Leu	Pro	Gly	Pro	Ala
				455				460						465
Glu	Pro	Pro	Gly	Leu	Pro	Pro	Ala	Ser	Leu	Pro	Glu	Ser	Thr	Pro
				470				475						480
Ile	Pro	Ser	Ser	Ser	Gln	Thr	Pro	Phe	Pro	Pro	His	Tyr	Leu	Arg
				485				490						495
Leu	Pro	Ser	Leu	Arg	Arg	Ser	Arg	Gln	Cys	Leu	Lys	Pro	Pro	Ala
				500				505						510
Arg	Gly	Pro	Pro	Pro	Pro	Pro	Trp	Asn	Cys	Trp	Pro	Pro		
				515				520						

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT12
- (B) CLONE: 3129120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77 :

Met	Gly	Leu	Leu	Ser	Asp	Pro	Val	Arg	Arg	Arg	Ala	Leu	Ala	Arg
					5			10						15
Leu	Val	Leu	Arg	Leu	Asn	Ala	Pro	Leu	Cys	Val	Leu	Ser	Tyr	Val
					20				25					30
Ala	Gly	Ile	Ala	Trp	Phe	Leu	Ala	Leu	Val	Phe	Pro	Pro	Leu	Thr
				35				40						45
Gln	Arg	Thr	Tyr	Met	Ser	Glu	Asn	Ala	Met	Gly	Ser	Thr	Met	Val
				50				55						60

Glu Glu Gln Phe Ala Gly Gly Asp Arg Ala Arg Ala Phe Ala Arg
 65 70 75
 Asp Phe Ala Ala His Arg Lys Lys Ser Gly Ala Leu Pro Val Ala
 80 85 90
 Trp Leu Glu Arg Thr Met Arg Ser Val Gly Leu Glu Val Tyr Thr
 95 100 105
 Gln Ser Phe Ser Arg Lys Leu Pro Phe Pro Asp Glu Thr His Glu
 110 115 120
 Arg Tyr Met Val Ser Gly Thr Asn Val Tyr Gly Ile Leu Arg Ala
 125 130 135
 Pro Arg Ala Ala Ser Thr Glu Ser Leu Val Leu Thr Val Pro Cys
 140 145 150
 Gly Ser Asp Ser Thr Asn Ser Gln Ala Val Gly Leu Leu Leu Ala
 155 160 165
 Leu Ala Ala His Phe Arg Gly Gln Ile Tyr Trp Ala Lys Asp Ile
 170 175 180
 Val Phe Leu Val Thr Glu His Asp Leu Leu Gly Thr Glu Ala Trp
 185 190 195
 Leu Glu Ala Tyr His Asp Val Asn Val Thr Gly Met Gln Ser Ser
 200 205 210
 Pro Leu Gln Gly Arg Ala Gly Ala Ile Gln Ala Ala Val Ala Leu
 215 220 225
 Glu Leu Ser Ser Asp Val Val Thr Ser Leu Asp Val Ala Val Glu
 230 235 240
 Gly Leu Asn Gly Gln Leu Pro Asn Leu Asp Leu Leu Asn Leu Phe
 245 250 255
 Gln Thr Phe Cys Gln Lys Gly Gly Leu Leu Cys Thr Leu Gln Gly
 260 265 270
 Lys Leu Gln Pro Glu Asp Trp Thr Ser Leu Asp Gly Pro Leu Gln
 275 280 285
 Gly Leu Gln Thr Leu Leu Leu Met Val Leu Arg Gln Ala Ser Gly
 290 295 300
 Arg Pro His Gly Ser His Gly Leu Phe Leu Arg Tyr Arg Val Glu
 305 310 315
 Ala Leu Thr Leu Arg Gly Ile Asn Ser Phe Arg Gln Tyr Lys Tyr
 320 325 330
 Asp Leu Val Ala Val Gly Lys Ala Leu Glu Gly Met Phe Arg Lys
 335 340 345
 Leu Asn His Leu Leu Glu Arg Leu His Gln Ser Phe Phe Leu Tyr
 350 355 360
 Leu Leu Pro Gly Leu Ser Arg Phe Val Ser Ile Gly Leu Tyr Met
 365 370 375
 Pro Ala Val Gly Phe Leu Leu Leu Val Leu Gly Leu Lys Ala Leu
 380 385 390
 Glu Leu Trp Met Gln Leu His Glu Ala Gly Met Gly Leu Glu Glu
 395 400 405
 Pro Gly Gly Ala Pro Gly Pro Ser Val Pro Leu Pro Pro Ser Gln
 410 415 420
 Gly Val Gly Leu Ala Ser Leu Val Ala Pro Leu Leu Ile Ser Gln
 425 430 435
 Ala Met Gly Leu Ala Leu Tyr Val Leu Pro Val Leu Gly Gln His
 440 445 450
 Val Ala Thr Gln His Phe Pro Val Ala Glu Ala Glu Ala Val Val
 455 460 465
 Leu Thr Leu Leu Ala Ile Tyr Ala Ala Gly Leu Ala Leu Pro His
 470 475 480
 Asn Thr His Arg Val Val Ser Thr Gln Ala Pro Asp Arg Gly Trp
 485 490 495
 Met Ala Leu Lys Leu Val Ala Leu Ile Tyr Leu Ala Leu Gln Leu
 500 505 510
 Gly Cys Ile Ala Leu Thr Asn Phe Ser Leu Gly Phe Leu Leu Ala

	515		520		525									
Thr	Thr	Met	Val	Pro	Thr	Ala	Ala	Leu	Ala	Lys	Pro	His	Gly	Pro
				530					535					540
Arg	Thr	Leu	Tyr	Ala	Ala	Leu	Leu	Val	Leu	Thr	Ser	Pro	Ala	Ala
				545					550					555
Thr	Leu	Leu	Gly	Ser	Leu	Phe	Leu	Trp	Arg	Glu	Leu	Gln	Glu	Ala
				560					565					570
Pro	Leu	Ser	Leu	Ala	Glu	Gly	Trp	Gln	Leu	Phe	Leu	Ala	Ala	Leu
				575					580					585
Ala	Gln	Gly	Val	Leu	Glu	His	His	Thr	Tyr	Gly	Ala	Leu	Leu	Phe
				590					595					600
Pro	Leu	Leu	Ser	Leu	Gly	Leu	Tyr	Pro	Cys	Trp	Leu	Leu	Phe	Trp
				605					610					615
Asn	Val	Leu	Phe	Trp	Lys									
				620										

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: HEARNOT01
- (B) CLONE: 305841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78 :

CCCTCGAGAA GATGGCGGCG ACTCTGGGAC CCCTTGGTC GTGGCAGCAG TGGCGGCGAT 60
 GTTTGTGGC TCGGGATGGG TCCAGGATGT TACTCCTTCT TCTTTGTTG GGGTCTGGC 120
 AGGGGCCACA GCAAGTCGGG GCGGGTCAA CGTCGAGTA CTTGAAACGG GAGCACTCGC 180
 TGTCGAAGCC CTACCAGGGT GTGGGCACAG GCAGTTCTC ACTGTGGAAT CTGATGGCA 240
 ATGCCATGGT GATGACCCAG TATATCCGCC TTACCCCCAGA TATGCAAAGT AAACAGGGTG 300
 CCTTGTGAA CCGGGTGCCA TGTTTCTGA GAGACTGGGA GTTGCAGGTG CACTTCAAA 360
 TCCATGGACA AGGAAAGAAG AATCTGCATG GGGATGGCTT GGCAATCTGG TACACAAAGG 420
 ATCGGATGCA GCCAGGGCCT GTGTTGGAA ACATGGACAA ATTTGTGGGG CTGGGAGTAT 480
 TTGTAGACAC CTACCCCAAT GAGGAGAACG AGCAAGAGCG GGTATTCCCC TACATCTCAG 540
 CCATGGTGA CAACGGCTCC CTCAGCTATG ATCATGAGCG GGATGGCGG CCTACAGAGC 600
 TGGGAGGCTG CACAGCCATT GTCCGCAATC TTCATTACGA CACCTTCCTG GTGATTCGCT 660
 ACGTCAAGAG GCATTTGACG ATAATGATGG ATATTGATGG CAAGCATGAG TGGAGGGACT 720
 GCATTGAAGT GCCCGGAGTC CGCCTGCCCG GCGGCTACTA CTTCGGCACC TCCTCCATCA 780
 CTGGGATCT CTCAGATAAT CATGATGTCA TTTCTTGAA GTTGTGAA CTGACAGTGG 840

PF-0459 US

AGAGAACCCC AGAAGAGGAA AAGCTCCATC GAGATGTGTT CTTGCCCTCA GTGGACAATA 900
TGAAGCTGCC TGAGATGACA GCTCCACTGC CGCCCCTGAG TGGCCTGGCC CTCTTCCTCA 960
TCGTCTTTT CTCCCTGGTG TTTCTGTAT TTGCCATAGT CATTGGTATC ATACTCTACA 1020
ACAAATGGCA GGAACAGAGC CGAAAGCGCT TCTACTGAGC CCTCCTGCTG CCACCACTTT 1080
TGTGACTGTC ACCCATGAGG TATGGAAGGA GCAGGGACTG GCCTGAGCAT GCAGCCTGGA 1140
GAGTGTCTT GTCTCTAGCA GCTGGTTGGG GACTATATTC TGTCACTGGA GTTTGAATG 1200
CAGGGACCCC GCATTCCCAT GGTTGTGCAT GGGGACATCT AACTCTGGTC TGGGAAGCCA 1260
CCCACCCAG GGCAATGCTG CTGTGATGTG CCTTCCCTG CAGTCCTTCC ATGTGGGAGC 1320
AGAGGTGTGA AGAGAATTAA CGTGGTTGTG ATGCCAAAT CACAGAACAG AATTCATAG 1380
CCCAGGCTGC CGTGGTTTT GACTCAGAAG GCCCTCTAC TTCAGTTTG AATCCACAAA 1440
GAATTAAAAA CTGGTAACAC CACAGGCTT CTGACCATCC ATTGTTGGG TTTGCATTT 1500
GACCCAACCC TCTGCCTACC TGAGGAGCTT TCTTGAAA CCAGGATGGA AACTCTTCC 1560
CTGCCTTACC TTCCTTCAC TCCATTCTT GTCCCTCTG TGTGCAACCT GAGCTGGAA 1620
AGGCATTTGG ATGCCTCTCT GTTGGGCCT GGGGCTGCAG AACACACCTG CGTTCACTG 1680
GCCTTCATTA GGTGGCCCTA GGGAGATGGC TTTCTGCTT GGATCACTGT TCCCTAGCAT 1740
GGGTCTTGGG TCTATTGGCA TGTCCATGGC CTTCCAATC AAGTCTCTC AGGCCCTCAG 1800
TGAAGTTGG CTAAAGGTTG GTGTAAAAAT CAAGAGAACG CTGGAAGACA TCATGGATGC 1860
CATGGATTAG CTGTGCAACT GACCAGCTCC AGGTTGATC AAACCAAAAG CAACATTGT 1920
CATGTGGTCT GACCATGTGG AGATGTTCT GGACTTGCTA GAGCCTGCTT AGCTGCATGT 1980
TTTGTAGTTA CGATTTTGG AATCCCACCT TGAGTGCTGA AAGTGTAAAGG AAGCTTTCTT 2040
CTTACACCTT GGGCTTGGAT ATTGCCAGA GAAGAAATT GGCTTTTT TTCTTAATGG 2100
ACAAGAGACA GTGCTGTT TCATGTTCCA AGTCTGAGAG CAACAGACCC TCATCATCTG 2160
TGCCTGGAAG AGTTCACTGT CATTGAGCAG CACAGCCTGA GTGCTGGCCT CTGTCAACCC 2220
TTATTCCACT GCCTTATTTG ACAAGGGGTT ACATGCTGCT CACCTTACTG CCCTGGGATT 2280
AAATCAGTTA CAGGCCAGAG TCTCCTTGGA GGGCCTGGAA CTCTGAGTCC TCCTATGAAC 2340
CTCTGTA 2347

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1529 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: EOSIHET02
(B) CLONE: 322866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79 :

CCACACGCGTC CGCCAGCCTT GTCTCGGCCA CCTCAAGGAT AATCACTAAA TTCTGCCGAA 60
AGGACTGAGG AACGGTGCCT GGAAAAGGGC AAGAATATCA CGGCATGGGC ATGAGTAGCT 120
TGAAACTGCT GAAGTATGTC CTGTTTCTC TCAACTTGCT CTTTGGATC TGTGGCTGCT 180
GCATTTGGG CTTTGGGATC TACCTGCTGA TCCACAACAA CTTCGGAGTG CTCTTCCATA 240
ACCTGCCCTC CCTCACGCTG GGCAATGTGT TTGTCATCGT GGGCTCTATT ATCATGGTAG 300
TTGCCTTCCT GGGCTGCATG GGCTCTATCA AGGAAAACAA GTGTCTGCTT ATGTCGTTCT 360
TCATCCTGCT GCTGATTATC CTCCTGCTG AGGTGACCTT GGCCATCCTG CTCTTGTAT 420
ATGAACAGAA GCTGAATGAG TATGTGGCTA AGGGTCTGAC CGACAGCATC CACCGTTACC 480
ACTCAGACAA TAGCACCAAG GCAGCGTGGG ACTCCATCCA GTCATTCTG CAGTGGTGTG 540
GTATAATGG CACGAGTGAT TTGGACAGTG GCTCACCCAGC ATCTTGCCTT TCAGATCGAA 600
AAAGTGGAGGG GTGCTATGCG AAAGAAGACT TTGGTTTCAT TCAATTTCCT GTATATCGGA 660
ATCATCACCA TCTGTGTATG TGTGATTGAG GTGTTGGGG ATGTCCTTG CACTGACCCCT 720
GAAGTGCAG ATTGACAAAAA CCAGCCAGAC CATAGGGCTA TGATCTGCAG TAGTTCTGTG 780
GTGAAGAGAC TTGTTTCATC TCCGGAAATG CAAAACCATT TATAGCATGA AGCCCTACAT 840
GATCACTGCA GGATGATCCT CCTCCCATCC TTTCCCTTT TAGGTCCCTG TCTTATACAA 900
CCAGAGAAGT GGGTGTGGC CAGGCACATC CCATCTCAGG CAGCAAGACA ATCTTCACT 960
CACTGACGGC AGCAGCCATG TCTCTCAAAG TGGTGAAACT AATATCTGAG CATTTTAG 1020
ACAAGAGAGG CAAAGACAAA CTGGATTAA TGGCCCAACA TCAAAGGGTG AACCCAGGAT 1080
ATGAATTTT GCATCTTCCC ATTGTCGAAT TAGTCTCCAG CCTCTAAATA ATGCCAGTC 1140
TTCTCCCCAA AGTCAAGCAA GAGACTAGTT GAAGGGAGTT CTGGGGCCAG GCTCACTGGA 1200
CCATTGTCAC AACCCCTCTGT TTCTCTTGA CTAAGTGCCC TGGCTACAGG AATTACACAG 1260
TTCTCTTCT CCAAAGGGCA AGATCTCATT TCAATTCTT TATTAGAGGG CCTTATTGAT 1320
GTGTTCTAAG TCTTCCAGA AAAAAACTAT CCAGTGATTT ATATCCTGAT TTCAACCAGT 1380
CACTTAGCTG ATAATCACAG TAAGAAGACT TCTGGTATTA TCTCTCTATC AGATAAGATT 1440
TTGTTAATGT ACTATTTAC TCTTCAATAA ATAAAACAGT TTATTATCTC AAAAAAAA 1500
AAAAAAAAA AAAAAAAA AAAAAAAA 1529

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BEPINOT01
- (B) CLONE: 546656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80 :

GCATCCCCGC TTCCGGGTTA GGCGTTCCT GCCCGCCCCC TCCTCTCCTC CCTTCGGACC 60
CATAGATCTC AGGCTCGGCT CCCCGCCCGC CGCAGCCCAC TGTTGACCCG GCCCGTACTG 120
CGGCCCCGTG GCCACCATGT CCCTGCACGG CAAACGGAAG GAGATCTACA AGTATGAAGC 180
GCCCTGGACA GTCTACGCGA TGAACCTGGAG TGTGCGGCCG GATAAGCGCT TTCGCTTGGC 240
GCTGGGCAGC TTCTGGGAGG AGTACAACAA CAAGGTTCAAG CTTGTTGGTT TAGATGAGGA 300
GAGTCAGAG TTTATTTGCA GAAACACCTT TGACCCACCA TACCCACCA CAAAGCTCAT 360
GTGGATCCCT GACACAAAAG GCGTCTATCC AGACCTACTG GCAACAAAGCG GTGACTATCT 420
CCGTGTGTGG AGGGTTGGTG AAACAGAGAC CAGGCTGGAG TGTTGCTAA ACAATAATAA 480
GAACCTGTGAT TTCTGTGCTC CCCTGACCTC CTTGACTGG AATGAGGTGG ATCCTTATCT 540
TTTAGGTACC TCAAGCATTG ATACGACATG CACCATCTGG GGGCTGGAGA CAGGGCAGGT 600
GTTAGGGCGA GTGAATCTCG TGTCTGGCCA CGTGAAGACC CAGCTGATCG CCCATGACAA 660
AGAGGTCTAT GATATTGCAT TTAGCCGGGC CGGGGGTGGC AGGGACATGT TTGCCTCTGT 720
GGGTGCTGAT GGCTCGGTGC GGATTTGA CCTCCGCCAT CTAGAACACA GCACCACAT 780
TTACGAAGAC CCACAGCATC ACCCACTGCT TCGCCTCTGC TGGAACAAAGC AGGACCCCTAA 840
CTACCTGGCC ACCATGGCA TGGATGGAAT GGAGGTGGTG ATTCTAGATG TCCGGGTTCC 900
CTGCACACCT GTCGCCAGGT TAAACAAACCA TCGAGCATGT GTCAATGGCA TTGCTGGC 960
CCCACATTCA TCCTGCCACA TCTGCACTGC AGCGGATGAC CACCAGGCTC TCATCTGGGA 1020
CATCCAGCAA ATGCCCGAG CCATTGAGGA CCCTATCCTG GCCTACACAG CTGAAGGAGA 1080
GATCAACAAT GTGCAGTGGG CATCAACTCA GCCCGACTGG ATCGCCATCT GCTACAACAA 1140
CTGCCTGGAG ATACTCAGAG TGTAGTGTG GTGGCGCTGT GCCCACGAGG CAGGGGCTT 1200
TGTATTCCT GCCTCTGCC CACCCCAAA GTAAGAAGAA ACATGTTCC AGTGGCCAGT 1260
ATGTCTTCA TTGCTTGCA CCCACTGTTA CCAGAAGCTG CTCTAGGAGT TCCTGGCCAG 1320

TCACCCCATC GCCCTCTGTG GCAGACTCAG TGCTGTGTGG CGCCTCCTCA GCCCAGGGCT 1380
 GAGTTTAAG ATTTCTCTC CTTTCCTCTT CTCCTTGTT TCCTCAATTA AAAAATGTGT 1440
 GTATATTGT TTGTCAGGCG TTGTGTTGAG GAGCAGTTCA CGCACTGGCT GTGTCTATTG 1500
 CTCTGCCAG GTGTCTCTGT TTGCTGCCCA AGGCAGCAGT TCATGTCTCG TCCATGTCCA 1560
 TGTCGTGTT AGCACTTACG TGGGAACAAA TACCAATTG TCTTTCTCC TAGTATCAGT 1620
 GTGTTAACAA AATTTAACT TTGTATATTT GTTATCTATC AGGCTAATTT TTTTATGAAA 1680
 AGAATTTAC TCTCCTGCTT CATTCTTTG TCTTATAGTC CTCCCTCTT GCACCTTCTT 1740
 CTCTCCCTC AGTGCCTGGA GCTGGTACTG GGCCCCTGGG CCCCATGAGC AGTTGCCTT 1800
 CTTGAGTCAC TGCCTGTGTA GTACATACCT GACCGGGAGT CCAAACCACC TTGGTGCTCT 1860
 GAAGTCCACT GACTCATCAC ACCTTTCTTA GCCTGGCTCC TCTCAAGGGC ATTCTGGGCT 1920
 TGAAACAGA CATAGGAAGC CTCTGTTTAC CCTGAAGCAC CACTGTCCAG CCCATTGGTT 1980
 CCCACTGGCA GCATGGTAGA GCTGAGAGAA ACAGGCTCTC AGGGTACCTG ACTTGAGGGG 2040
 AATCGTTCA TGAAGCTGAA CTTCAAGCAT ATTTCCAGTA CATTCTTCA GAGTCTGTTT 2100
 TTCCATCCAA ATATAAGCCC CAGGCCATTG CACTTAGTGT CTTTCAATG ATAGGCAAGA 2160
 ATGATATCTG AGTTGAACCTT CGGTGCTTCT GTTGTGTTGAG TTTACTGTGC CTGGTGGTAT 2220
 ATTGGCATT CTTGGATTG AGTGTCTGA GGTGAGAGAG TCTTCCCGAG GCATCCTGTC 2280
 TGTGCTTCCA ACCCTGAACA AGACCTTACA TGAGAGATGG ACTGATGGAC TGCGGCAATC 2340
 CTGGGCTGTC AAGTGGATAG ATAGTTAAA AGCATTATAC TGTGGTAAT GAAAAGGGAG 2400
 GAAAAAAA GAAGGAAAAG GAATTATAGA CCCCCAGGGT CAGCCAGTTA AGAGCTCTAC 2460
 CCACACCTGT CAACCCCTCT CTCCCCCAGT TTAGGTTCTG AGCAGTATTG GACTTGTAGC 2520
 CTGCAGTTGT CTTTGACTT GCAGGCCGCA GGTGTCTTTC TGTTATGTGA ATGAGTTCCA 2580
 TGGAGGGGCA TATGTGTGAT TCCACCGTTA GATGAGCCCT TGGGGCAGGC AGTTTGGGAT 2640
 GTGCTCTGG GGGAAAGTTG GCTGTTCTC TGCGCTCTGC TCCTACCCGA AGGTTTTAA 2700
 GTCCCTCTGA ATTGCTCATC TGAGATTAGT AGAGTAGCAG GCCTGAAGGA TGATGGTTT 2760
 GTCCTCTTG GTTCTCACCT GCTTGAGAAG TAAAACAGTA ACTTTGTTCT TCTGGGCCCT 2820
 TAAGCTTTT TGTTAAAGTC TTCCTTTCA GAAGTAGATG TCATTATATG CCAAAAGTCT 2880
 AGCTCTTGC TTTACCATAC AGGGACCTGT CCCAAAGAAA AAGGCTCTT TTTAGGCCAG 2940
 CATATTCCTT CTTCTACCCCT TTTACTTTGT TGTTCTGATT TTAGGACTCT GGCTGGCCAT 3000
 GTGCTTGTGG TTGCCTCTCC TGCATTTGCC ACTGGATTG CACTGCATCG TTTGGAGATA 3060
 CAAAGCGAGC AGTTCTGGT CAGAACCCCTC CTCTGCTTTT CATTGTGTTT GATAATGGTT 3120
 ACTGGGCCTT TCTCTCAAGG GTAGCAAGGC CAAGCTGATG GCTGCTTGTGTT TAGGAGGCCA 3180

PF-0459 US

TCAGTTCTT CCTGTGGAGA AGGGTCTGAA ATGGAAGTCA GTGGTAGAAG GGGCTGGTCT 3240
GCTGGGCAGG GCTTACATCC ACTGAGTTCT AAGATTCTT TCCTGATCTG CACCTACGCC 3300
TGGTCTGTAT GGTGGAATTG GTCAGCTGGA ACTCAGAAAC AACAAACTTGA AAAAAAAAATA 3360
ATAATTAGAA CATATTTGCA TAAGATAGCT ATTTACTCTG GAAACCAACA ACTTTGAGA 3420
TTTCCCTTGC CCTGTGGACG CCCAGCTCCT GTCATCCTTC CTTAGGTCT GCAGTACAGT 3480
CTTCCCTGAA ATGCCACCGG GGACCCAGGG GGACTCCACC CCCCTAAGCA AGCACACACA 3540
TACTCACAGT TGATGAGTTG CTGGTCTTTG AGTCCCAGCT CTCTTACCCCT CCCTTTACTC 3600
CACCAAGCCCCG ACGACCCATG ACTGAGGAGG GGATTTCTAC AGTCTCAGGA TTTAGAAAGT 3660
CTGTAAGCCA TCCATGCTCC AGAAAGCACC GATCTGTTGT AGTTGCAAAA ACAACTCTGT 3720
AATTGTTGA GGTTCTCAAA CTGACAGCCA GCGAGACTGG GTGGGAGGCC CTGGATCTGT 3780
TCTCCCTGAC TGCAGGGAGGA GCAGCCACTA GGACTTTAGC AGGAAGCCCA CATGGAGGCT 3840
CCGCCAGGCT GTGGCCCAGC TGGTGATGGC CCTTTGCTC CTGGCAGCCT GAGGCACAGC 3900
TGCCTGTATT GTCCTCATCT GTTCTGACTG AAGGATGGAG GTGCTGAATA AATTAGGCCT 3960
CAGGCCTCTA CCACCCAGAGA GCTGGAGAAT GGGTCCACGT CATTCAAGGA CCTGAATT 4020
TTATGCTCAG GAGCATTGGA ATCCTCTTCT TCCAGGGAGG AATTAGCCTG CAAGGTTAGG 4080
ACTTGAAGAG GGAAGGTATT TAATAACTGG GCGAGGATGG GTGTGGTGGC TCACACCTGT 4140
AATCCCAGCA TTTTGGGAGG CTGAGGTGGC CAGATCCAA GGTCAGAAGA TCGAGACCCT 4200
CCTGGCTAAC ATGGTGAAC CCCATCTCTA CTAAAAATAC AAAAAAAAT TAGCCGGGG 4260
TGGTGGCGGG TACCTGTAGT CCTAGCTACT TGGGAGGCTG AGGCAGGAGA ATGGCGTGAA 4320
CCTGGGAGGT GGAGCTTGCA GTGAGCCAAG ATCGTCCACT CACTGCAGCC TGGCGACAGA 4380
GCAAGCG 4387

(2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2117 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: SYNORAT03
 - (B) CLONE: 693453
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81 :

GCCTGAGCGG GAAGCATTGG CGTCCGAGCG ACTTCTAGGA GCCTGGGGTT CGGCGCTATG 60

GAGGAGCTCG ATGGCGAGCC AACAGTCACT TTGATTCCAG GCGTGAATTC CAAGAAGAAC 120
 CAAATGTATT TTGACTGGGG TCCAGGGGAG ATGCTGGTAT GTGAAACCTC CTTCAACAAA 180
 AAAGAAAAAT CAGAGATGGT GCCAAGTTGC CCCTTTATCT ATATCATCCG TAAGGATGTA 240
 GATGTTTACT CTCAAATCTT GAGAAAACTC TTCAATGAAT CCCATGGAAT CTTTCTGGC 300
 CTCCAGAGAA TTGACGAAGA GTTGACTGGA AAATCCAGAA AATCTCAATT GGTCGAGTG 360
 AGTAAAAACT ACCGATCAGT CATCAGAGCA TGTATGGAGG AAATGCACCA GGTTGCAATT 420
 GCTGCTAAAG ATCCAGCCAA TGGCCGCCAG TTCAGCAGCC AGGTCTCCAT TTTGTCAGCA 480
 ATGGAGCTCA TCTGGAACCT GTGTGAGATT CTTTTTATTG AAGTGGCCCC AGCTGGCCCT 540
 CTCCTCCTCC ATCTCCTTGA CTGGGTCCGG CTCCATGTGT GCGAGGTGGA CAGTTGTCG 600
 GCAGATGTTT TGGGCAGTGA GAATCCAAGC AAACATGACA GCTTCTGGAA CTTGGTGACC 660
 ATCTTGGTGC TGCAGGGCCG GCTGGATGAG GCCCGACAGA TGCTCTCCAA GGAAGCCGAT 720
 GCCAGCCCCG CCTCTGCAGG CATATGCCGA ATCATGGGG ACCTGATGAG GACAATGCC 780
 ATTCTTAGTC CTGGGAACAC CCAGACACTG ACAGAGCTGG AGCTGAAGTG GCAGCACTGG 840
 CACGAGGAAT GTGAGCGGTA CCTCCAGGAC AGCACATTG CCACCAGCCC TCACCTGGAG 900
 TCTCTTTGA AGATTATGCT GGGAGACGAA GCTGCCTTGT TAGAGCAGAA GGAACATTCTG 960
 AGTAATTGGT ATCATTTCCT AGTGACTCGG CTCTTGTACT CCAATCCAC AGTAAAACCC 1020
 ATTGATCTGC ACTACTATGC CCAGTCCAGC CTGGACCTGT TTCTGGAGG TGAGAGCAGC 1080
 CCAGAACCCC TGGACAACAT CTTGTTGGCA GCCTTGAGT TTGACATCCA TCAAGTAATC 1140
 AAAGAGTGCA GCATCGCCCT GAGCAACTGG TGGTTGTGG CCCACCTGAC AGACCTGCTG 1200
 GACCACTGCA AGCTCCTCCA GTCACACAAAC CTCTATTTCG GTTCCAACAT GAGAGAGTC 1260
 CTCCTGCTGG AGTACGCCTC GGGACTGTT GCTCATCCCA GCCTGTGGCA GCTGGGGTC 1320
 GATTACTTTG ATTACTGCC CGAGCTGGC CGAGTCTCCC TGGAGCTGCA CATTGAGCGG 1380
 ATACCTCTGA ACACCGAGCA GAAAGCCCTG AAGGTGCTGC GGATCTGTGA GCAGCGGCAG 1440
 ATGACTGAAC AAGTCGAG CATTGTAAG ATCTTAGCCA TGAAAGCCGT CCGCAACAAT 1500
 CGCCTGGGTT CTGCCCTCTC TTGGAGCATC CGTGCTAAGG ATGCCGCCTT TGCCACGCTC 1560
 GTGTCAGACA GGTTCCTCAG GGATTACTGT GAGCGAGGCT GCTTTCTGA TTTGGATCTC 1620
 ATTGACAACC TGGGCCAGC CATGATGCTC AGTGACCGAC TGACATTCCCT GGGAAAGTAT 1680
 CGCGAGTTCC ACCGTATGTA CGGGGAGAAG CGTTTGCCG ACGCAGCTTC TCTCCTTCTG 1740
 TCCTTGATGA CGTCTCGGAT TGCCCCCTCGG TCTTTCTGGA TGACTCTGCT GACAGATGCC 1800
 TTGCCCCCTT TGGAACAGAA ACAGGTGATT TTCTCAGCAG AACAGACTTA TGAGTTGATG 1860
 CGGTGTCTGG AGGACTTGAC GTCAAGAAGA CCTGTGCATG GAGAATCTGA TACCGAGCAG 1920

PF-0459 US

CTCCAGGATG ATGACATAGA GACCACCAAG GTGGAAATGC TGAGACTTTC TCTGGCACGA 1980
AATCTTGCTC GGGCAATTAT AAGAGAAGGC TCACTGGAAG GTTCCTGAGA ACTGCTTCAA 2040
TGTGGTATCT TTGTATGGCA ATGTATATAG ATTTTTAAA AGAATAAAATG TTGTTTGCAA 2100
AAAAAAAAAAA AAAAAAA 2117

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 846 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: BRAITUT03
(B) CLONE: 866885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82 :

GGCGGGCGGA GTCTGCAGGA TGGCACCGGA CCCCTGGTTC TCCACATACG ATTCTACTTG 60
TCAAATTGCC CAAGAAATTG CTGAGAAAAT TCAACAAACGA AATCAATATG AAAGAAAAGG 120
TGAAAAGGCA CCAAAGCTTA CCGTGACAAT CAGAGCTTG TTGCAGAACC TGAAGGAAAA 180
GATGCCCTT TTGAAGGACT TATTGCTAAG AGCTGTGTCA ACACATCAGA TAACACAGCT 240
TGAAGGGGAC CGAACAGACA ACCTCTTGA TGATCTTGTA ACTCGAGAGA GACTACTTCT 300
GGCATCCTT AAGAATGAGG GTGCCGAACC AGATCTAATC AGGTCCAGCC TGATGAGTGA 360
AGAGGCTAAG CGAGGAGCAC CCAACCCCTG GCTCTTGAG GAGCCAGAGG AGACCAGAGG 420
CTTGGTTTT GATGAAATCC GGCAACAGCA GCAGAAAATT ATCCAAGAAC AGGATGCAGG 480
CCTTGATGCC CTTCCCTCTA TCATAAGTCG CCAAAAACAA ATGGGGCAGG AAATTGGGAA 540
TGAATTGGAT GAACAAAATG AGATAATTGA CGACCTTGCC AACCTAGTGG AGAACACAGA 600
TGAAAAACTT CGCAATGAAA CCAGGCGGGT AAACATGGTG GACAGAAAGT CAGCCTCTG 660
TGGGATGATC ATGGTGATTT TACTGCTGCT TGTGGCTATC GTGGTTGTTG CAGTCTGGCC 720
GACCAACTGA TGGCAGTAAA GAGACCACCA GCAGTGACAC CTGGCAATGA CAGATGCAAG 780
CCCAACACCC TTTGGTACG CAAAACCTGC TCTCAATAAA TTCCCCAAA GCTCTGAAAA 840
AAAAAA 846

(2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1011 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: LUNGNOT03
 - (B) CLONE: 1242271

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83 :

GAAAGAGATA ACTGGAAGTT CCTTGATTCA GAAAACAGAT TCAGATGAAG AAGTTGCAAT 60
GCTGTTGGAC ACAGTCCAGA AAGTATTCA GAAAATGTTG GAATGTATTG CACGGAGCTT 120
CAGGAAGCAG CCGGAAGAAG GCCTGCGGCT GCTTTATTCT GTTCAGAGGC CTCTTCATGA 180
GTTCATTACT GCTGTTCACT CTCGGCACAC AGACACCCCT GTGCACCGGG GTGTACTTC 240
TACTCTGATC GCTGGGCCTG TGGTTGAGAT AAGTCACCAG CTACGGAAGG TTTCTGACGT 300
AGAAGAGCTT ACCCCTCCAG AGCATCTTC TGATCTTCCA CCATTTCAA GGTGTTAAT 360
AGGAATAATA ATAAAGTCTT CGAATGTGGT CAGGTCAATT TTGGATGAAT TAAAGGCATG 420
TGTGGCTTCT AATGATATTG AAGGCATTGT GTGCCTCACG GCTGCTGTGC ATATTATCCT 480
GGTTATTAAT GCAGGTAAAC ATAAAAGCTC AAAAGTGAGG GAGGTTGCAG CCACTGTTCA 540
CAGAAAACTA AAGACATTCA TGGAAATTAC TTTGGAAGAG GATAGCATTG AAAGATTTCT 600
CTATGAATCA TCATCAAGAA CTCTGGAGA ACTTTGAAT TCATAACCAA GCCAACATCT 660
CCAGACATGT AAAAATAGGG AAAAGTGATT CAAATTGAAA TGCCTGTGA TTTTCCTATT 720
GTTTTTAATG TTAATAACCC ATATAATAGG GAAAGGGTGG GATTTTTTG TGGGAATGTG 780
GGAAGGTGGG GGTTATGGAG GAGATAACTC AAAACTTCTT CAATTTGCC TAGTGCCTGC 840
GTAAATAATA TATTTAATAT AAAGGACTCC AGGTATGAAT GGTGTAGAAA TCCATGATTC 900
CAAGAAAAAA CACTTTCTA GCAAACCTGG TTGTTTTAA AATGACTTT ATATATGTAA 960
TATTGCTTGG AAACTATGAG TAATAAAGCA ATGACAACAT CAAAAAAA A 1011

- (2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2478 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: LUNGFET03
 - (B) CLONE: 1255027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84 :

CCCACGCGTC CGCCCACGCG TCCGCAGCGC TGTGTTGCG AGCGGGAGCG AGGGGCGCCG 60
GCTGGGGTGT GTGCTCCTGA GCTCTTCAGA AACCAGGCTG CTTTCAGGAA CATTGCTGTG 120
GATTCCCAGC TTTCAGACAA CACATGACTA AGACAGATGA GACCACTCTA GTTGCCTCAT 180
GGGAAACTCG GGAAAAGACT GCAAAAACAA CATTGTTCT CCCTTGAA TTCTGGAGTT 240
ATAAGGCAGA GGTCCCCAT CTTCCCGAAC TGGCCTATTC CGCTAGAAGC AAGATGGCTG 300
AACTCAATAC TCATGTGAAT GTCAAGGAAA AGATCTATGC AGTTAGATCA GTTGTTCCTA 360
ACAAAAGCAA TAATGAAATA GTCCTGGTGC TCCAACAGTT TGATTTAAT GTGGATAAAG 420
CCGTGCAAGC CTTTGTGGAT GGCAGTGCAA TTCAAGTTCT AAAAGAATGG AATATGACAG 480
GCAAAAAGAA GAACAATAAA AGAAAAAGAA GCAAGTCAA GCAGCATCAA GGCAACAAAG 540
ATGCTAAAGA CAAGGTGGAG AGGCCTGAGG CAGGGCCCT GCAGCCGCAG CCACCACAGA 600
TTCAAAACGG CCCCATGAAT GGCTGCGAGA AGGACAGCTC GTCCACAGAT TCTGCTAACG 660
AAAAACCAGC CCTTATCCCT CGTGAGAAAA AGATCTCGAT ACTTGAGGAA CCTTCAAAGG 720
CACTTCGTGG GGTACAGCAA GGCAACAGAC TACTGCAACA GAAACTATCC TTGATGGGA 780
ACCCCAAACC TATACATGGA ACAACAGAGA GGTCAAGATGG CCTACAGTGG TCAGCTGAGC 840
AGCCTTGTAA CCCAAGCAAG CCTAAGGCAA AAACATCTCC TGTAAAGTCC AATACCCCTG 900
CAGCTCATCT TGAAATAAAG CCAGATGAGT TGGCAAAGAA AAGAGGCCA AATATTGAGA 960
AATCAGTGAA GGATTGCAA CGCTGCACCG TTTCTCTAAC TAGATATCGC GTCATGATTA 1020
AGGAAGAAGT GGATAGTTCC GTGAAGAAGA TCAAAGCTGC CTTGCTGAA TTACACAAC 1080
GCATCATTGA CAAAGAAGTT TCATTAATGG CAGAAATGGA TAAAGTTAAA GAAGAAGCCA 1140
TGGAAATCCT GACTGCTCGT CAGAAGAAAG CAGAAGAACT AAAGAGACTC ACTGACCTTG 1200
CCAGTCAGAT GGCAGAGATG CAGCTGGCCG AACTCAGGGC AGAAATTAAG CACTTTGTCA 1260
GCGAGCGTAA ATATGACGAG GAGCTCGGG AAGCTGCCG GTTTCCTGT GACATCGAAC 1320
AGCTGAAGGC CCAAATCATG CTCTGCGGAG AAATTACACA TCCAAAGAAC AACTATTCC 1380
CAAGAACTCC CTGCAGCTCC CTGCTGCCTC TGCTGAATGC GCACGCAGCA ACCTCTGGGA 1440
AACAGAGTAA CTTTCCCGA AAATCATCCA CTCACAATAA GCCCTCTGAA GGCAAAGCGG 1500
CAAACCCCAA AATGGTGAGC AGTCTCCCCA GCACCGCCGA CCCCTCTCAC CAGACCATGC 1560
CGGCCAACAA GCAGAATGGA TCTTCTAACCC AAAGACGGAG ATTTAATCCA CAGTATCATA 1620
ACAACAGGCT AAATGGGCCT GCCAAGTCGC AGGGCAGTGG GAATGAAGCC GAGCCACTGG 1680
GAAAGGGCAA CAGCCGCCAC GAACACAGAA GACAGCCGCA CAACGGCTTC CGGCCAAAAA 1740
ACAAAGGCAGG TGCCAAAAAT CAAGAGGCTT CTTGGGGAT GAAGACCCCC GAGGCCCGG 1800

PF-0459 US

CCCATTCCTGA AAAGCCCCGG CGAAGGCAGC ACGCTGCAGA CACCTCGGAG GCCAGGCCCT 1860
TCCGGGGTAG TGTCCGTAGG GTTTCACAGT GCAATCTCTG CCCCACGAGA ATAGAAGTTT 1920
CCACAGATGC AGCAGTTCTC TCAGTCCCGG CTGTGACGTT GGTGGCCTGA GCTAGGAGGA 1980
AAAAGAGCAG TTTTCACTCA GTTTGGTTT CCTGCCCGAG GTGCTGACCC AATTGCTGC 2040
CAAAAGAGTG TCAATCAGAA TATACAAATC CCGTATGGTT GTGTCATCCT CTCTTAATCA 2100
TTTTTACTAA TTCTAATAAT CAGCTCTAGC TTGCTTCATA ATTTCATGG CTTTGCTTGA 2160
TCTGTTGATG CTTCTCTCA TCAAGACTTT GCAGCATTTC AGCCAGGCAG TATTACTCA 2220
TTATTAGGAA AATCAAGATG TGGCTGAAGA TCAGAGGCTC AGTTAGCAAC CTGTGTTGTA 2280
GCAGTGATGT CAGTCCATTG ATTGTCTTA GAGAGTTAAT GTTACAAAAAA AGAATTCTTA 2340
ATAATCAGAC AACATGATC TGCTGAGGAC ACATGCGCTT TTGTAGAATT TAACATCTGG 2400
TGTTTTCTG AAAAAATATA TATACATATA TTGCTTTATT TGAAACAAAT TAAAATATGC 2460
TGCATTTGAA AAAAAAAA 2478

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1897 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: TESTTUT02
(B) CLONE: 1273453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85 :

TGCACATCTA GCACAAATTG AAGATGATAG AGCTGCGATG GTTATTCTT GGCATCTGGC 60
AAGTGACATG GACTGTGTAG TCACCCCTAAC CACTGACGCT GCACGTCGTA TCTATGATGA 120
AACCCAAGGT CGTCAGCAGG TGTTGCCCT TGATTCTATT TACAAGAAGA CTCTCCAGA 180
TTGGAAAAGA TCTCTACCTC ATTTCCGAAA TGGAAAATTG TATTTAAAC CCATTGGAGA 240
TCCAGTCTT GCTCGAGACT TGTAAACATT TCCAGATAAT GTAGAACATT GTGAAACAGT 300
ATTTGGTATG CTGTTAGGAG ACACCATTAT TTTGGATAAT CTGGATGCGG CCAATCATT 360
TAGAAAAGAG GTGTTAAAA TTACACACTG TCCTACACTG CTGACCAGAG ATGGAGATCG 420
AATTGAAAGT AATGGAAAGT TTGGGGCCCT TCAGAATAAA GCTCCTCCAA TGGATAAACT 480
TCGGGGAATG GTATTGGAG CTCCAGTTCC AAAACAGTGT CTGATCTTAG GGGAACAAAT 540
AGATCTTCTT CAGCAGTATC GTTCTGCTGT GTGCAAACTA GACAGTGTGA ATAAGGATCT 600

TAAACAGTCAA TTAGAGTACC TTCGCACCTCC GGATATGAGG AAGAAAAAGC AAGAACTTGA 660
 TGAACATGAG AAAAATCTCA AACTAATAGA GGAAAAACTA GGTATGACTC CCATACGTAA 720
 GTGTAATGAC TCATTGCGTC ATTCAACCAAA GGTGAGACG ACAGATTGTC CAGTTCCTCC 780
 TAAAAGAATG AGACGAGAAG CTACAAGACA AAATAGGATT ATAACCAAAA CAGATGTATG 840
 AGAGGTGACA GAGAGAAGAG GCCATTGGTC TCAGTAAGAA TGCCCTGCTT TCTGCATCTC 900
 TGTTTCAGAA GACCAAGAGG GTGACTTACC AGACTGAGTA TTTCTGGGA CAATACAAGT 960
 ACCTGGGCAT GAATTCCAT TTCGATTCAAG ATGGGACTGG AAACAACCAT TCAATTTAT 1020
 GAATCTTACT GGACATTATG GATTTACTGG AATTATTCCA GACATTATGC CCTTTGGTTG 1080
 TCACTACCTT GCAAATGTGT AAGAGGAAA TGTGCTAATG TGGCAGTGAC TGTAAAACGT 1140
 GCACATGGCA TTTATTAATC CTGAAGAAAA GTACATGTAC TATTTTCAG TATAAAATATA 1200
 ATGAACATGT CAGAACTATT TCTTGAAAC CTTTTTATTA CTTTGCCTG AATTTATTAA 1260
 ACAAAAGATGT TTTGTCTTT GTGTAAGGGA GGTTCTAGAG GCTAGATGTT TAATTGTAAA 1320
 TATGTGAGGA AACTCAATGC AGAATTCAAG ATAAAAAATT TAAAAGCACA GGTATTTGGG 1380
 AATTGAAATG TTAAGATACC CAGAACAAACA TTAAATCAAT GAGTGAACCT GTGACAGTGG 1440
 TAGCATTCA AATTCAAAA GACTTATCCT GTGTGTGTGT GTGTGTGTGT ATATATATAT 1500
 ATATATATAT AAATATATAT ATATAAAATA TTCAGCAGCA CCAAGTTTA TAACTATTGT 1560
 TTGTTTGACT TTATTAATAC TAGAATATGT AGTCTCAGCC TTAATTTAC ATTTACATTA 1620
 TTTTGTATT TTTTATTACT ATTTTAAGG GGTAAAGAG AACATACATT CTCACATTAG 1680
 TGTACTTTCT GGTAGAAAGT TGCTGCAAAA ACATTTGAAA TGTATATTAA CCTAATGTAT 1740
 GTCATATATA TGTCTTGTG TAAGTTCAAG ACTATTGATC TGTGAAGTTA TTTTGTAAAGG 1800
 ACATACATTG GGTAAGTAAG TTTGTGTCCC AGGAAATGTA TGTGTTTTA AACCCTTCT 1860
 AAATATGCAG GCCATTAATA AATAAGATTG TGTCTCA 1897

(2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1488 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: TESTTUT02
 - (B) CLONE: 1275261

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86 :

PF-0459 US

CCCCACGCGTC CGGGGACATC CTGTTCTGAG TCAAGATTCC TCCTTCTGAA CATGGGACTT 60
TCCAGAAAGGA CCACAGCTCC TCCCCTGCAT CCACTCGGCC TGGGAGGTTC TGGATTTGG 120
CTGTCGAGGG AGTTTGCCTG CCTCTCCAGA GAAAGATGGT CATGAGGCCCT GTGAGGAGTC 180
TGCTTCTCTG GGAAGCCCTA CTTCCCATTAG CAGTTACTGG TGCCCAAGTG CTGAGCAAAG 240
TCGGGGGCTC GGTGCTGCTG GTGGCAGCGC GTCCCCCTGG CTTCCAAGTC CGTGAGGCTA 300
TCTGGCGATC TCTCTGGCCT TCAGAAGAGC TCCTGGCCAC GTTTTCCGA GGCTCCCTGG 360
AGACTCTGTA CCATTCCCGC TTCCTGGGCC GAGGCCAGCT ACACAGCAAC CTCAGCCTGG 420
AGCTCGGGCC GCTGGAGTCT GGAGACAGCG GCAACTTCTC CGTGTGATG GTGGACACAA 480
GGGGCCAGCC CTGGACCCAG ACCCTCCAGC TCAAGGTGTA CGATGCAGTG CCCAGGCCCG 540
TGGTACAAGT GTTCATTGCT GTAGAAAGGG ATGCTCAGCC CTCCAAGACC TGCCAGGTTT 600
TCTTGTCCCTG TTGGGCCCCC AACATCAGCG AAATAACCTA TAGCTGGCGA CGGGAGACAA 660
CCATGGACTT TGGTATGGAA CCACACAGCC TCTTCACAGA CGGACAGGTG CTGAGCATT 720
CCCTGGGACC AGGAGACAGA GATGTGGCCT ATTCCCTGCAT TGTCTCCAAC CCTGTCAGCT 780
GGGACTTGGC CACAGTCACG CCCTGGGATA GCTGTCATCA TGAGGCAGCA CCAGGGAAGG 840
CCTCCTACAA AGATGTGCTG CTGGTGGTGG TGCCCTGTCTC GCTGCTCCTG ATGCTGGTTA 900
CTCTCTTCTC TGCCTGGCAC TGGTCCCCCT GCTCAGGGAA AAAGAAAAAG GATGTCCATG 960
CTGACAGAGT GGGTCCAGAG ACAGAGAACCC CCGTTGTGCA GGATCTGCCA TAAAGGACAA 1020
TATGAACTGA TGCCTGGACT ATCAGTAACC CCACTGCACA GGCACACGAT GCTCTGGAC 1080
ATAACTGGTG CCTGGAAATC ACCATGGTCC TCATATCTCC CATGGGAATC CTGTCCTGCC 1140
TCGAAGGAGC AGCCTGGGCA GCCATCACAC CACGAGGACA GGAAGCACCA GCACGTTCA 1200
CACCTCCCCC TTCCCTCTCC CATCTTCTCA TATCCTGGCT CTTCTCTGGG CAAGATGAGC 1260
CAAGCAGAAC ATTCCATCCA GGACACTGGA AGTTCTCCAG GATCCAGATC CATGGGGACA 1320
TTAATAGTCC AAGGCATTCC CTCCCCCACC ACTATTCTA AAGTACTAAC CAACTGGCAC 1380
CAAGAAAAAA TCCTCACTAA CCGCATCATC CGACAACTAA TAATTACAC TACATCCAAA 1440
CATCACTTAG CGGGCGGGGC CGCCGACTGG TTCCGGGCTT AGGGTGGG 1488

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: COLNNOT16
 (B) CLONE: 1281682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87 :

CCGACTTTGT AGCATTTTA TTTAAGCTAA AACAGAGCAC ATGTATATGT ACATAAGACA 60
 CATTAATCT ATAAATACTA TTTATTCACTT TTATATAAAC TAATGTAATG GAAAACAAAT 120
 TCTTATGACT TTGTGGTTT ATAGATGTT TAGAAACTTT GTATGTAGGT ATCTACAAA 180
 TTAGTTCACTT CCCCTGAATA TTTTGCAATT CATATTTTG AGGTCTTGAT GTTTTCAGCC 240
 TCTGGCGAAT CTTTTCAATT GAATTTGAAC CATTGTAAA ATCTGTGATG CTGAAGCAGA 300
 GTGTGTCACA AAGTGATGAG AACATTACTA AAATCCACGG ACGCACTGCG ACCTAAGGGC 360
 TCAACGGCTG ACTCGGCAGC GGGCAGCCAC CCCACGCTCC CCTGCGGTCA CTCGCACACC 420
 ACAGCCTGAA GCTCCCCCAG CGCCTGCACC TCGCACACAG CTAAGGTCAA AGTTCAAACG 480
 CACTCCACAC GGAAGCTCAT TCTATACCCG AAGAGCAGTC TCAGAAAGCA AGATTACTTT 540
 TGTGTTTTT AAAAAATGAT TCTTTAATGT ATTTTTCTAA ACATTCTGAT TGGAAGTAGT 600
 GGATTCCCAA ATGATTCCAA AGTCATCTGT AATTCTTCTG TTTTGTTT GTTCTGTCTT 660
 TTCTTCATT TGGCTTGAGG TGGGGGGAGG GGCAGGTGAC ACAAAGGATT TTTTTTTTT 720
 TTTTTTTTA ATTTTGAA TCTTTCCAA TAACCAGCTA AAGATTGCA CTGAAATACA 780
 ACTTGTATGC CTTTGCATT TTTAAAGCCT GCTTCCTGGA TTTAAGCAGA GTGATAGTGT 840
 TCAAAGAGCC AGTCAGCCT GTAACATATT TGAAAAAGAT ATGTCTGCAC TTTGAGGTCC 900
 CTTTGAATG CCATTCACTA GACCTCTCAA GCATTTGTT TCATTGCTAC ATCCAAGCGC 960
 CTCACAAGTC CACAATGCGG GACAGCATCA AAAGCTCAAG ACTTTGGAAA AAGCTTGTGG 1020
 GCTTGCAGTG GGGGAGGGAA GGGAACAAAA TTTGTGTACT TCTTTGTTA ATTTAGAAAT 1080
 AAGGCATCCA AGAGATGCCA TTATTTCTG TGTTTCAATT GTTGTGCCTT TGAGTTAAC 1140
 TGCATTTTG TCTTTGGTT GAAATCTGAA ATGTAATGTC CCAATATAAA ACAGTAATTAA 1200
 TTTGACCTTT GCAGTGTGTT TCTGGTCCTT TTCAGTTGA TTGCATATAA ATGTGGAAC 1260
 TGATAGATCT CTATATTTT AATGCACTTG TGATAAACTG GCAGCAGGGT TAGACATTAC 1320
 TTTCAAAGCT TGAGGTAGAC CGAGTCAGCA TGCTAGA 1357

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2330 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: BRSTNOT07
(B) CLONE: 1298305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88 :

CCTACTTGTGTT CCCACCTTGG GAGAGGACGA TGACTTGGGA GGGACCGCTG AAGGGAGAAG 60
GGGTCCCTCCC ATGAGGCTGA GGATGGCCTG AACCTGGAGC AGCGGACCAG GCAGACGGGC 120
TGAAGTGGGG TCCCAAATTC CATGTCCAGA GGTGTGGGG A GCCTGCCTCC CTAGCTCCTG 180
GCCCTGCCA GGGGCTTACA TCAAAACACC TCAGAGGGCT GCCCTCCAGA GGCTGCACCC 240
AGAACAGTGG GACATGAGCA GGGGTGTGGG CTTGGAGGGT GAAGAGGGATG TGGTCCTATC 300
AGATGCTGGG CCTCCTCAGC CATAGCCCCC TGCTCCTACC CCCTGACTGG CTCTTGTGTC 360
CTCACCTCTC ACCCTCTCCT TCCTGGGAGG CCCTGGGAGG TGATCATTGA CACCCAGCCA 420
AGCAGACAGC TGCGGGTGCC CAAGCCCTTG CTGGGCCTGC GCGTGAGGAG TCCCACGTGCT 480
TCTAAAGGAA GTCCTGGCA GGAGGTGGCT TTGGTGGTTG GTTCCAAAGT TGAAAATGCT 540
TGCAGTTGA CCTTAGAAGA AGTGGGAAGA AGAAGGAGCT CTACAGGGTC AGCTTTGTTT 600
GATTGTCCA GTCTAAGAAG TCCCATTGCC AAAGCTTCT GCAGGAGGGT GAATGCCGCA 660
GCTTGGCAGC CCCTGGTTT CTCTGGAAA TGGTCAGTTT CCCCTCAAAG TACCCAAAGT 720
AGCCTTGGCT TGAGTTTTG TCCTGCCTC CTTTTAGAG AAGAGGGCAT TTAGACTGCA 780
TTTCCTGGT TAAAGAAGGT TAAAGCAAAT GTTTATTGCC TTTCTAGTG AACTAACTCG 840
TAGAGATGTT CTCAGCAGGA AGACAGTCTT AGCACTGTCA CTTAGCAGAT TGCACCTAAC 900
TCCCTGTGC TGGCCAGATG GCGTGGCTGG TTGCCTTAAT ATGTCCCAGG ACCCCTGACA 960
GGGCTGCCTG GCCTCTCCCT CGTGCTCCTC AAGAGCCCAG TCCATACACT GTGGATGTCA 1020
TTGCTGTCGG GTTAGGAAGT CTTGTCCTAG AACGCCCTGG CTGGTATGAC CACAGTTCAT 1080
GGCGGCTCTT CTCGCTGGG TCATGGTCAT CTTCCAGCAC CTGCTGTGCT GGGAAAGGCCG 1140
AGGATGGGGG CCCAGCACTG TCCAGGCCTG CTGGGGCCTG GCTGGGAGTC CTGTGGGCAG 1200
CATGGAACAT GCAGCTGGC TTCCTGTGAC CAGGCACCCCT CTGGCACTGT TGCTTGCCT 1260
GTGCCCTGGA CCTTTCTCG CCCTCTCCT TCCTCTGCTC CCTTGGGGCT ACCCCTTGGC 1320
CCCTCCTGGT CTGTGCAAAC TCCCTCAGGG AGCCCCCTG CCCTGTAGCT CTCACCTAAC 1380
TTCCTAGGGG CTGCTGAGCC CACCCAGAGG TTGTTGGAGT TCAGGGGGC AGCTTGTCTC 1440
CCTTGTCAAGC AGGGCGTAA GGGCTGGTT TGGCCATACA AGGTTGGCTA CGCCCTCAAT 1500
CCCTGACCGT TCCAGGCACT GAGCTGGCA CCCACGGAAG GACATGCTGT CCAGACTGTG 1560

ATGACTGCCA GCACAGGGCA TCTCGGGCTT GGCTGGTCTG CGAGGCCTTG CCCCTGTGGA 1620
ACTCTGGGTT CCTGTTTCT CAGTCTTTT GC GGCTTTGC TGTGGTTGGC AGCTGCCGTA 1680
CTCCAGGCTT GTGTCGGCCA CTCAGATGAG GGCTGTGGTG CGAGCCAGTG CAGGAGAGCT 1740
GCGCTTGGGA TTGTGCCCTC TCCTGTGTCT GTCCTCCGGA CCTACCCAGG TCTCCACCAT 1800
CAGGACCCTG TCTTGGGTT TAGAAGACCA AGTATGGGGA AAACCAGACA CCAGCCTCTG 1860
CAGCAATGGG TCCCTCTAGC CTGTGGACAC CAGCTGGGGG ATCCAGGGTC AGGCCCCCTC 1920
CTCTCCCCAG TTTCCCTCTG CTGTGGGTT TC GGCTGTCA TGTCTCCACC ACTTAAGGAT 1980
GTCTTTACAC TGACTTCAGG ATAGATGCTG GGATGCCTGG GCATGCCAC ATGTTACATG 2040
TACAGAACTT TGTCTACAGC ACAAAATTAAG TTATATAAAC ACAGTGACTG GTATTTAATG 2100
CTGATCTACT ATAAGGTATT CTATATTAT ATGACTTCAG AGACCGGTAT GTAATAAAGG 2160
ACGCCCTCCC TCCAGTGTCC ACATCCAGTT CACCCCAGAG GGTCGGGCAG GTTGACATAT 2220
TTATTTTGT CTATTCTGTA GGCTTCCATG TCCAGAATCC TGCTTAAGGT TTTAGGGTAC 2280
CTTCAGTACT TTTTGCATAA AAAGTATTC CTATCCAAAA AAAAAAAA 2330

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2729 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: LUNGNOT12
(B) CLONE: 1360501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89 :

CTACACCTTT TCCATTTGCT AATAAGGCC CGCCAGGCTG GGAGGGATT GTCCCTGCCT 60
GCTTCTGGAG AAAGAAGATA TTGACACCCT CTACGGGCAC CATGGAACAG CACAGGTGTT TTAGAGGCAG 120
CCATTCTTT TCTTCTGCC AGTATTTGCA GCAGTAACAG CACAGGTGTT TTAGAGGCAG 180
CTAATAATTCT ACTTGTTGTT ACTACAACAA AACCACATCTAT AACAAACACCA AACACAGAAAT 240
CATTACAGAA AAATGTTGTC ACACCAACAA CTGGAACAAC TCCTAAAGGA ACAATCACCA 300
ATGAATTACT TAAAATGTCT CTGATGTCAA CAGCTACTTT TTTAACAAAGT AAAGATGAAG 360
GATTGAAAGC CACAACCACT GATGTCAGGA AGAATGACTC CATCATTCA AACGTAACAG 420
TAACAAAGTGT TACACTTCCA AATGCTGTTT CAACATTACA AAGTTCCAAA CCCAAGACTG 480
AAACTCAGAG TTCAATTAAA ACAACAGAAA TACCAGGTAG TGTTCTACAA CCAGATGCAT 540

CACCTTCTAA AACTGGTACA TTAACCTCAA TACCAGTTAC AATTCCAGAA AACACCTCAC 600
AGTCTCAAGT AATAGGCAC T GAGGGTGGAA AAAATGCAAG CACTTCAGCA ACCAGCCGGT 660
CTTATTCCAG TATTATTTG CCGGTGGTTA TTGCTTGAT TGTAATAACA CTTTCAGTAT 720
TTGTTCTGGT GGGTTGTAC CGAATGTGCT GGAAGGCAGA TCCGGGCACA CCAGAAAATG 780
GAAATGATCA ACCTCAGTCT GATAAAGAGA GCGTGAAGCT TCTTACCGTT AAGACAATT 840
CTCATGAGTC TGGTGAGCAC TCTGCACAAG GAAAAACCAA GAACTGACAG CTTGAGGAAT 900
TCTCTCCACA CCTAGGCAAT AATTACGCTT AATCTTCAGC TTCTATGCAC CAAGCGTGG 960
AAAGGAGAAA GTCCTGCAGA ATCAATCCCG ACTTCCATAC CTGCTGCTGG ACTGTACCAG 1020
ACGTCTGTCC CAGTAAAGTG ATGTCCAGCT GACATGCAAT AATTGATGG AATCAAAAAG 1080
AACCCCGGGG CTCTCCTGTT CTCTCACATT TAAAAATTCC ATTACTCCAT TTACAGGAGC 1140
GTTCCCTAGGA AAAGGAATT TAGGAGGAGA ATTTGTGAGC AGTGAATCTG ACAGCCCAGG 1200
AGGTGGGCTC GCTGATAGGC ATGACTTTCC TTAATGTTA AAGTTTCCG GGCCAAGAAT 1260
TTTATCCAT GAAGACTTTC CTACTTTCT CGGTGTTCTT ATATTACCTA CTGTTAGTAT 1320
TTATTGTTA CCACTATGTT AATGCAGGGA AAAGTTGCAC GTGTATTATT AAATATTAGG 1380
TAGAAATCAT ACCATGCTAC TTTGTACATA TAAGTATTAA ATTCCCTGCTT TCGTGTACT 1440
TTAATAAAAT AACTACTGTA CTCAAACTC TAAAAAACT ATAACATGAC TGTGAAAATG 1500
GCAATGTTAT TGTCTTCCTA TAATTATGAA TATTTTGGA TGGATTATTA GAATACATGA 1560
ACTCACTAAT GAAAGGCATT TGTAATAAGT CAGAAAGGGA CATAGGATTC ACATATCAGA 1620
CTGTTAGGGG GAGAGTAATT TATCAGTTCT TTGGTCTTTC TATTTGTCAT TCATACTATG 1680
TGATGAAGAT GTAAGTGCAA GGGCATTAT AACACTATAC TGCATTTCATT AAGATAATAG 1740
GATCATGATT TTTCATTAAC TCATTTGATT GATATTATCT CCATGCATTT TTTATTTCTT 1800
TTAGAAATGT AATTATTTGT TCTAGCAATC ATTGCTAAC TCTAGTTGT AGAAAATCAA 1860
CACTTTATAA ATACATAATT ATGATATTAT TTTTCATTGT ATCACTGTTC TAAAAATACC 1920
ATATGATTAT AGCTGCCACT CCATCAGGAG CAAATTCTTC TGTTAAAAGC TAACTGATCA 1980
ACCTTGACCA CTTTTTGAC ATGTGAGATC AAAGTGTCAA GTTGGCTGAG GTTTTTGGA 2040
AAGCTTTAGA ACTAATAAGC TGCTGGTGGC AGCTTTGTA CGTATGATTA TCTAAGCTGA 2100
TTTGATGCT AAATTATCTT AGTGATCTAA GGGGCAGTTT AGTGAAGATG GAATCTTGTA 2160
TTTAAAATAG CCTTTAAAAA TTTGTTTGT GGTGATGTAT TTTGACAAC TCCATCTTA 2220
GGAGTTATAT AATCACCTTG ATTTAGTTT CCTGATGTTT GGACTATTTA TAATCAAGGA 2280
CACCAAGCAA GCATAAGCAT ATCTATATTT CTGACTGGTG TCTCTTGAG AAGGATGGGA 2340
AGTAGAAAAA AAAAAAAGAA AGAAAGGAAA GGAAGAGAGG AGAGAAGAAG GCAGGGATCT 2400

CCACTATGTA TGTTTCACT TTAGAACTGT TGAGCCCATG CTTAATTAA ATCTAGAAGT 2460
CTTTAAATGG TGAGACAGTG ACTGGAGCAT GCCAATCAGA GAGCATTGT CTTCAGAAAA 2520
AAAAAAAATC TGAGTTGAG ACTAGCCTGG CCAACATGTT GAAACCCAT ATCTACTAAA 2580
AATACAAAAA TTAGCCTGGT GTGGTGGCGC ACGCCTGTAG TCCCAGCTAC TCTGGAGCCT 2640
GAGGAACGTG AATCGCTTGA ACCCAGAAGA CAGAGGTTGC AGTGAGCTGA GATGGCACTA 2700
TTGCACTCCA GACTGGTGAC ACACGCAGA 2729

(2) INFORMATION FOR SEQ ID NO: 90:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: LUNGNOT12
(B) CLONE: 1362406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90 :

GGCCCCTGCA CTGCTCCTGA TCCCTGCTGC CCTCGCCTCT TTCATCCTGG CCTTTGGCAC 60
CGGAGTGGAG TTCGTGCGCT TTACCTCCCT TCGGCCACTT CTTGGAGGGA TCCCGGAGTC 120
TGGTGGTCCG GATGCCCGCC AGGGATGGCT GGCTGCCCTG CAGACCGCAG CATCCTTGCC 180
CCCCTGGCAT GGGATCTGGG GCTCCTGCTT CTATTTGTTG GGCAGCACAG CCTCATGGCA 240
GCTGAAAGAG TGAAGGCATG GACATCCGG TACTTTGGGG TCCTTCAGAG GTCACTGTAT 300
GTGGCCTGCA CTGCCCTGGC CTTGCAGCTG GTGATGCGGT ACTGGGAGCC CATAACCCAAA 360
GGCCCTGTGT TGTGGGAGGC TCGGGCTGAG CCATGGGCCA CCTGGGTGCC GCTCCTCTGC 420
TTTGTGCTCC ATGTCATCTC CTGGCTCCTC ATCTTAGCA TCCTTCTCGT CTTTGACTAT 480
GCTGAGCTCA TGGGCCTCAA ACAGGTATAC TACCATGTGC TGGGGCTGGG CGAGCCTCTG 540
GCCCTGAAGT CTCCCCGGGC TCTCAGACTC TTCTCCCACC TGCGCCACCC AGTGTGTGTG 600
GAGCTGCTGA CAGTGTGTG GGTGGTGCCT ACCCTGGCA CGGACCGTCT CCTCCTTGCT 660
TTCCTCCTTA CCCTCTACCT GGGCCTGGCT CACGGGCTTG ATCAGCAAGA CCTCCGCTAC 720
CTCCGGGCC AGCTACAAAG AAAACTCCAC CTGCTCTCTC GGCCCCAGGA TGGGGAGGCA 780
GAGTGAGGAG CTCACTCTGG TTACAAGCCC TGTTCTTCCT CTCCCAGCTGA ATTCTAAATC 840
CTTAACATCC AGGCCCTGGC TGCTTCATGC CAGAGGCCA AATCCATGGA CTGAAGGAGA 900
TGCCCCTTCT ACTACTTGAG ACTTTATTCT CTGGGTCCAG CTCCATACCC TAAATTCTGA 960

PF-0459 US

GTTCAGCCA CTGAACCTCA AGGTCCACTT CTCACCAGCA AGGAAGAGTG GGGTATGGAA 1020
GTCATCTGTC CCTTCACTGT TTAGAGCATG ACACTCTCCC CCTCAACAGC CTCCTGAGAA 1080
GGAAAGGATC TGCCCTGACC ACTCCCCCTGG CACTGTTACT TGCCTCTGCG CCTCAGGGT 1140
CCCCCTCTGC ACCGCTGGCT TCCACTCCAA GAAGGTGGAC CAGGGTCTGC AAGTTCAACG 1200
GTCATAGCTG TCCCTCCAGG CCCCAACCTT GCCTCACCAAC TCCCAGGCCCT AGTCTCTGCA 1260
CCTCCTTAGG CCCTGCCTCT GGGCTCAGAC CCCAACCTAG TCAAGGGGAT TCTCCTGCTC 1320
TTAACTCGAT GACTTGGGGC TCCCTGCTCT CCCGAGGAAG ATGCTCTGCA GGAAAATAAA 1380
AGTCAG 1386

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 542 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: LATRTUT02
(B) CLONE: 1405329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91 :

CCCGGGCCAT GCAGCCTCGG CCCCAGGGC GCCCGCCGCG CACCCGAGGA GATGAGGCTC 60
CGCAATGGCA CCTTCCTGAC GCTGCTGCTC TTCTGCCTGT GCGCCTTCCT CTCGCTGTCC 120
TGGTACGCCG CACTCAGCGG CCAGAAAGGC GACGTTGTGG ACGTTTACCA GCGGGAGTTC 180
CTGGCGCTGC GCGATCGGTT GCACGCAGCT GAGCAGGAGA GCCTCAAGCG CTCCAAGGAG 240
CTCAACCTGG TGCTGGACGA GATCAAGAGG GCGTGTCAAG AAAGGCAGGC GCTGCGAGAC 300
GGAGACGGCA ATCGCACCTG GGGCCGCCTA ACAGAGGAGC CCCGATTGAC GCCGTGGAAC 360
GGCTCACACC GGCACGTGCT GCACCTGCC ACCGTCTTCC ATCACCTGCC ACACCTGCTG 420
GCCAAGGAGA GCAGTCTGCA GCCCGCGGTG CGCGTGGGCC AGGGCCGCAC CGGAGTGTG 480
GTGGTGATGG GCATCCCGAG CGTGCAGCGC GAGGTGCACT CGTACCTGAC TGACACTCTG 540
CA 542

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: BRAINOT12
 - (B) CLONE: 1415223

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92 :

CGAGCCCCGA GTGCGGACAC CCCCGGGATG CTTGCGCCCC AGAGGACCCG CGCCCCAAGC 60
CCCCCGCGCCG CCCCCCAGGCC CACCCGGAGC ATGCTGCCTG CAGCCATGAA GGGCCTCGGC 120
CTGGCGCTGC TGGCCGTCCT GCTGTGCTCG GCGCCCGCTC ATGGCCTGTG GTGCCAGGAC 180
TGCACCCCTGA CCACCAAAC TC CAGCCATTGC ACCCCAAAGC AGTGCCAGCC GTCCGACACG 240
GTGTGTGCCA GTGTCCGAAT CACCGATCCC AGCAGCAGCA GGAAGGATCA CTCGGTGAAC 300
AAGATGTGTG CCTCCTCCTG TGACTTCGTT AAGCGACACT TTTTCTCAGA CTATCTGATG 360
GGGTTTATTA ACTCTGGGAT CTTAAAGGTC GACGTGGACT GCTGCGAGAA GGATTTGTGC 420
AATGGGGCGG CAGGGGCAGG GCACAGCCCC TGGGCCCTGG CCGGGGGGCT CCTGCTCAGC 480
CTGGGGCCTG CCCTCCTCTG GGCTGGGCC TGATGTCTCC TGCTTCCCAC GGGGCTTCTG 540
AGCTTGCTCC CCTGAGCCTG TGGCTGCCCT CTCCCCAGCC TGGCGTGGCT GGGGCTGGGG 600
GCAGCCTTGG GCCAGCTCCG TGGCTGTGGC CTGTGGGTCT GAATTCTTCC CCGACGTGAA 660
GCCTNCCTGT CTCTCCGGCA GCTCTGAGTC CCAGGCAGCT GGACATTCCA GGGGAACAAG 720
CCATTNGGCA GGAGGGCTGG GATGAGGTTG GGGGGGACCG GAGGTCCCGG AG 772

- (2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1738 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: BRAINOT12
 - (B) CLONE: 1416553

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93 :

TGTCCATCCA AAAACCATAA AATCACTGGG TTCCACATCA GCCTCCATGA GGCCAAGCCT 60
TGTACCTGCA AGCTCTTGGC CTAACCATTC CTCTGTCTC TTCTCTGGCC TGCCTGGGA 120
GCCCGTGAAG GCCGCACGGG TGCCTCCAGC CTGAGACATC AGGGGAGAGC CTGCAGCTGA 180

GTTCAGCAGA AAGGAGGAAT CCTGGCCCTC AGGAAGAAGA TAGTCACATG TTTTTCTTCC 240
 TTGTCCCCAC AGCCCCAGA ACAACATTCT CCCTGCTGGC AGCCCTTCCA TGTCTCCAAA 300
 CCTGGGTCAG AGTGAAAGGA CCTTTGGGG TGGGTGGGAG CAAAGGGCCC ACCTGCTGGT 360
 TGGTGAAAGC AGTGGTGCCG GAGTGCTAGG TACCGCACGA GTAGTGGTGC GGGGGCTTGG 420
 GAAGCAGACC AGGGTTGGAC AAAACCCAT GAGGGCGGGG AGCTGGAAGA AAAGTCTCTT 480
 GGGGACCTCT GGGGCAAGGA GCTGAGAAGT CCTGCAGCAC CAGGTGAGAC TTGCTTACAG 540
 TGGATGCCAC TTCTAGGCCT CTGGACCGCA GATGCCCTCC TCCCTCCTGC ACACCTGGCC 600
 TCCTGGGCCT CCAGGTAAAG AGAGAGAGCC AGCCCAGCCC TGTTCCCT CAGTCCTCCT 660
 TTGCTCCTGC TGCTTCTCCC AACAGCCAC TGTTAGGAGG TAGTAGACCC CAGCCTCAAG 720
 GCTCTGACCT TCTTCATGTG GGCACAGAGG GTCTGACAC TCTGGCAGGG CCTGAGCTGG 780
 GGCAGGCCTC CCTCAGGGCC AGGGGCGATG GCACCCCGGG GACAGGCAGA CCTCCTTCCT 840
 GCCGTCAGCA CCCCCCTTCCT TATCACTGTC TGGTCTCCGA GCTTCGGCTG CAGCCTGAGG 900
 TGTGTCCTGG GCTCCTCAGA GCCTGAAGCA AGCTTTGGA AGCCTGCAGT CCTCCCAGCT 960
 CCAGTGCAGA AGCCTCTCTC TCCAGCCTT CCCCAGGCAG GAGTTGGGT TGGGGGCCTC 1020
 TGTCCCTCAT CGCTTACCTT GGAAAGGTGG GAAGCTGGCA ATCTGCACCT TGGGGCCTGG 1080
 GCTCCCCCTC TCTGTGCCAG CGGCTTCCA GCACCTGGGA GGGGCTGCAG CCCCAGCTGG 1140
 ACTCCAGCCT GTCCCTCTTA GCACTCTAGC TGCCCACCTCC AGGGCAGGGA CTCGAAACCC 1200
 CCTCCGTCTT GAGCAGCCAC CTCCAGGGCC CTGTTGGGA CCACTCTCTC AGTCCCCAGG 1260
 TCCTCAGGGC CCCAGAGCGG GAGGGTCTCC TACCTGGAAG TCCCCCTGAG CTCCAGGGCC 1320
 CAGCCCTACC TGCCAGTGCT GGTGTAGGG CACTCAACAC CGAGTGTGGG GGCCACGCC 1380
 CTTGCCATGC CCACGGCCTC CTCCTGTAGC CCCTGCCTGC ACCCACGATG CTGCACGGGC 1440
 CCGCCCTGGT GGGGCTCGGC GAGTAATGTG TTTTGTCCCC AGTTAACAC CATTCTGCGG 1500
 CCTGGTTCTG CAAGGAACCA GGGCTGCCCT ACCGCCCCGCC GTCTGCCGCC CTAGGCTTCC 1560
 TGACTCCATT AGTTCCGACA CTTGTAAAC TCCGAGAAGT GCTGTGGTCT CAGCAATGCA 1620
 CCTGTTTGT ACATGATTGT GTAATTTAAA GGTATATAAA TACAAATATA TATATATATC 1680
 AGTTGTGATT GTATGACTGT GGATAAAATC CAGAACTGTG TCAACCTGAA AAAAAAAA 1738

(2) INFORMATION FOR SEQ ID NO: 94:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2100 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: KIDNNNOT09
(B) CLONE: 1418517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94 :

GGGAAAGCGG CGAGTAAGAT GGAAGATGAG GAGGTCGCTG AGAGCTGGGA AGAGGCGGCA 60
GACAGCGGGG AAATAGACAG ACGGTTGGAA AAAAAACTGA AGATCACACA AAAAGAGAGC 120
AGGAAATCCA AATCTCCTCC CAAAGTGCC CATTGTGATT AGGACGATAG CCTTCCCGCG 180
GGGCCCCCTC CACAGATCCG CATCCTCAAG AGGCCCACCA GCAACGGTGT GGTCAGCAGC 240
CCCAACTCCA CCAGCAGGCC CACCCTCCA GTCAAGTCCC TAGCACAGCG AGAGGCCGAG 300
TACGCCGAGG CCCGGAAGCG GATCCTGGC AGGCCAGCC CCGAGGAGGA GCAGGAGAAA 360
CCCATCCTCG ACAGGCCAAC CAGGATCTCC CAACCCGAAG ACAGCAGGCA GCCCAATAAT 420
GTGATCAGAC AGCCTTGGG TCCTGATGGG TCTCAAGGCT TCAAACAGCG CAGATAAATG 480
CAGGCAAGAA AAGATGCCGC CGTTGCTGCC GTCACCGCCT CCTGGGTCGT CCGCCACGGG 540
TTGCACTGCC GTGGCAGACA GCTGGACTTG AGCAGAGGGA ACGACCTGAC TTACTTGCAC 600
TGTGATCCCC CTTGCTCCGC CCACTGTGAC CTTGAACCCC ATGCACTGTG ACCTCCCCCC 660
TTCTCCCCCT TCCCACGTG ATTGGCACAT CGACAAGGGC TGTCCAAGT CAATGGAAAG 720
GGAAAGGGTG GGGGTTAGGG GAAGGTTGGG GGGACCCAGC AAGGACTCAG AGAGTCAGAC 780
AGTGCCACTT GGCCACTTGG GGTAAAGCCA GTGCCAGCAA TAACAGTTA TCATGCTCAT 840
TAATTTGGGA TTTCAAAACA CAAATGAAAAA CTCACACCCA CCCACCCCCA AGTGCATGTC 900
TCCATCACTT AAAAAGTAAG TTCCATTGAA AAATATCCTT TCTTTTTTT TTCTTCCTAT 960
TTTTGTTGT TTATACAAAT ATCTGATTG CAAGAAAAAG TGCATGGGAG GGGTTTAGT 1020
GGTTTAATGA ATTTTAATT AAGAAAGGGT AGTTGGTAG TCTACTTAA AATGTTCTG 1080
GGAAATTACAC TAGAAACATT AACCAATAGG ATTTGGTGA GCTTAGCTTC TGTATTCTA 1140
CTGCCGCCA GAAAAGGGC AGGGCTCTGC AGCCGCCAGG ACAGACGAGC ACCCCATGCC 1200
TATACCTCCC TCCCCGAGCT AAGTCCCAGG GCATCTGGC CTTGCCTGGA GACTGGGCTA 1260
GCTCTGTAGG CTCGGAGAGC CTGGGGAGGG TGCCAACCCC ACCTCTAGTA TTTGGGAGA 1320
TAGGGAAAGT GAACCGACTT CCCCTTCCA TACCCCTCAG GGTGGTCCC TACCAAGCCAG 1380
GCTTACTACT TCTAGAAGAA AGCAGAGTGC CAGGGAGTGA GATTGCATCC CTGGGCTTAG 1440
AAGTGACGGA GAGAAGACTT GTTTAGTATT TTGCCATCAG CACAAGGAAA ACCAGGAGAG 1500
AGTCTGCCTC CAGGACTCTG AGCCTCTGC CTCGTATGTT CAGAAGGTGG ATAGGTCTTC 1560

CCACTCCAGC ATGGCTTGAA CTCTTAGGGG TCTGCAGTGC TCCATCTCCA TTGGTGGCCC 1620
CAGCTCAGTA ACTATACCTG GTACATTCC TGTGTGCAAT CAGTACCTTG AAGGCAGAAC 1680
ATTCTGAATA AAGTTGGAAA AAGAACAGCT TTGCTTGCA AAGATTGATG ACAGACTGGT 1740
TCCTCAGAGG CCTAGGCTAC CCGTCACCCC TTTTCCAGA GCGAGGGCCT GGAATGAAGG 1800
CAGTTTATCC TCTGTCCCTG GAGCCTGGGG TTTGCTTTGG CTCCTTGAGG TGGAAGAGAC 1860
TAAGAGGGCA GCTGCCAGA GCAGCTGTGT GTACCTGGCT CCTCTCAGGC TTCTGATCC 1920
CTTCCATTGC ACTGCGCCTT ATCCCTCAGC CAGCCAGACA GCCTCCCTGC TCCTGACCAG 1980
CAGATACGTT TCGGAGTGGT TGGTGTGGTT TTTGTGATGA GGGCAGCACA TGGTGGCCAA 2040
GGTGGGCAAA GCTGAGTCTC ACAAGGCTCA AATCCCTTCG GTTGGGNTCC CCTTGTGGGG 2100

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2458 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: PANCNOT08
(B) CLONE: 1438165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95 :

GCAGGGCGGAG ATGTAGACCC GGTAGTGTG TGCTTGTGG TGACAACCTGG CGGCAGCGCG 60
CCGCGGGCCC GAGACTTAGT CTCGGGCCGC CATGGCCAGC GTCCACGAGA GCCTCTACTT 120
CAATCCCAGT ATGACCAATG GGGTTGTGCA CGCCAATGTG TTCGGCATCA AGGACTGGGT 180
GACGCCGTAC AAGATCGCGG TGCTGGTGCT GCTGAACGAG ATGAGCCGCA CAGGCGAGGG 240
CGCCGTCAGC CTCATGGAGC GGCGGAGGCT CAACCAGCTG CTCCTGCCCG TGCTGCAGGG 300
CCCAGATATT ACACGTCAA AACTTACAA GTTAATTGAA GAGTCTTGTC CACAGCTGGC 360
AAATTCACTG CAGATCAGAA TCAAAACTGAT GGCTGAAGGC GAGTTGAAGG ATATGGAACA 420
GTTTTTGAT GACCTTCAG ATTCTTCTC TGGAACGTAA CCAGAGGTTC ACAAAACAAG 480
TGTAGTAGGT TTGTTCTGC GTCACATGAT CTTGGCCTAC AGTAAGCTTT CTTTCAGCCA 540
AGTGTAACTG CCCTTCAGCA GTACTTCCAG AATGGTGAGA AAAAGACAGT 600
GGAGGATGCT GATATGGAAC TGACCAGTAG AGATGAGGGT GAAAGAAAAA TGGAAAAAGA 660
AGAACTTGAT GTATCTGTAA GAGAAGAGGA GGTATCTTGC AGTGGGCCTC TGTCCCAAAA 720
ACAAGCAGAA TTTTTCTTT CTCAACAGGC TTCTTGCTA AAGAATGATG AGACTAAGGC 780

PF-0459 US

CCTCACTCCA GCTTCCTTGC AGAAGGAATT AAACAATTG TTGAAATTG ATCCTGATT 840
TGCTGAAGCG CATTATCTCA GCTACTTAAA CAACCTCCGT GTCCAAGATG TTTTCAGTTC 900
AACACACAGT CTCCTCCATT ATTTGATCG TCTGATTCTT ACCGGAGCCG AAAGCAAAAG 960
TAATGGGAA GAGGGCTATG GCCGGAGCTT GAGATACGCC GCTCTGAATC TTGCCGCCCT 1020
GCACTGCCGC TTCGGTCACT ATCAACAGGC AGAGCTCGCC CTGCAGGAGG CAATTAGGAT 1080
TGCCCAGGAG TCCAACGATC ACGTGTGTCT CCAGCACTGT TTGAGCTGGC TTTATGTGCT 1140
GGGGCAGAAG AGATCCGATA GCTATGTTCT GCTGGAGCAT TCTGTGAAGA AGGCAGTACA 1200
TTTTGGGTTA CCGAGAGCTT TTGCTGGAA GACGGCAAAAC AAGCTGATGG ATGCCCTAAA 1260
GGACTCCGAC CTCCTGCACT GGAAACACAG CCTGTCAGAG CTCATCGATA TCAGCATCGC 1320
ACAGAAAACG GCCATCTGGA GGCTGTATGG CCGCAGCACC ATGGCACTGC AACAGGCCA 1380
GATGTTGCTG AGCATGAACA GCCTGGAGGC GGTGAATGCG GGCGTGCAGC AGAACAAACAC 1440
AGAGTCCTTT GCTGTCGCAC TCTGCCACCT CGCAGAGCTA CACGCGGAGC AGGGCTGTTT 1500
TGCTGCAGCT TCTGAAGTGT TAAAGCACTT GAAGGAACGA TTTCCGCCTA ATAGTCAGCA 1560
CGCCCAGTTA TGGATGCTAT GTGATCAAAA AATACAGTTT GACAGAGCAA TGAATGATGG 1620
CAAATATCAT TTGGCTGATT CACTTGTAC AGGAATCACA GCTCTCAATA GCATAGAGGG 1680
TGTTTATAGG AAAGCGGTTG TATTACAAGC TCAGAACCAA ATGTCAGAGG CACATAAGCT 1740
TTTACAAAAA TTGTTGGTTC ATTGTCAGAA ACTGAAGAAC ACAGAAATGG TGATCAGTGT 1800
CCTACTGTCC GTGGCAGAGC TGTACTGGCG ATCTTCCTCC CCTACCATCG CGCTGCCCAT 1860
GCTCCTGCAG GCTCTGGCCC TCTCCAAGGA GTACCGGTTA CAGTACTTGG CCTCTGAAAC 1920
AGTGCTGAAC TTGGCTTTG CGCAGCTCAT TCTTGGAAATC CCAGAACAGG CCTTAAGTCT 1980
TCTCCACATG GCCATCGAGC CCATCTTGGC TGACGGGGCT ATCCTGGACA AAGGTCGTGC 2040
CATGTTCTTA GTGGCCAAGT GCCAGGTGGC TTCAGCAGCT TCCTACGATC AGCCGAAGAA 2100
AGCAGAAGCT CTGGAGGCTG CCATCGAGAA CCTCAATGAA GCCAAGAACT ATTTTGCAAA 2160
GGTTGACTGC AAAGAGCGCA TCAGGGACGT CGTTTACTTC CAGGCCAGAC TCTACCATAC 2220
CCTGGGAAAG ACCCAGGAGA GGAACCGGTG TCGATGCTC TTCCGGCAGC TGCATCAGGA 2280
GCTGCCCTCT CATGGGGTAC CCTTGATAAA CCATCTCTAG AGAGGACATC CCTGCTGGC 2340
TGCTGTGCAG AGTATAAGAT TTTGGACTTG TTCATGTCCC CTCTCTCCCT ATAAATGATG 2400
TATTTGTGAC ACCCTATCTT GTCAATAAAC AGCATTCTGA TTAAAAAAA AAAAAAAA 2458

(2) INFORMATION FOR SEQ ID NO: 96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2900 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: THYRNOT03
 - (B) CLONE: 1440381

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96 :

TGCATGGATG GGATACTGGA TGAATCTTG CTTGAAACCT GTCCAATTCA GTCACCATTA 60
 CAAGTTTTG CAGGAATGGG TGGACTGGCT CTTATTGCTG AAAGACTACC CATGCTATAT 120
 CCAGAAGTAA TTCAACAGGT GAGTGCTCCA GTTGTAAACAT CTACCACTCA GGAAAAGCCG 180
 TATGATAGCG ATCAGTTGA ATGGGTGACC ATTGAACAGT CAGGGGAGTT AGTTTATGAA 240
 GCACCAGAAA CTGTTGCGGC TGAACCTCCA CCTATCAAGT CAGCAGTACA GACCATGTCT 300
 CCCATACCTG CCCATTCTTT GGCTGCTTTT GGATTATTTC TTCGTCTTCC GGGCTATGCG 360
 GAAAGTGTAC TGAAAGAGAG AAAACATGCC CAGTGCCTTC TTGATTGGT ATTGGGAGTG 420
 ACAGATGATG GAGAAGGAAG TCATATTCTT CAATCTCCAT CAGCCAATGT GCTTCCAACC 480
 CTTCTTCC ACGTCCTTCG TAGCTTGTTC AGCACTACAC CTTTGACAAC TGATGATGGT 540
 GTACTTCTAA GGCAGATGGC ATTGGAAATT GGAGCCTTAC ACCTCATTCT TGTCTGTCTC 600
 TCTGCTTGA GCCACCATTG CCCACGAGTT CCAAACCTCTA GCGTGAATCA AACTGAGCCA 660
 CAGGTGTCAA GCTCTCATAA CCCTACATCA ACAGAAGAAC AACAGTTATA TTGGGCCAAA 720
 GGGACTGGCT TTGGAACAGG CTCTACAGCT TCTGGGTGGG ATGTGGAACA AGCCTTAAC 780
 AAGCAAAGGC TGGAAAGAGGA ACATGTTACC TGCCTTCTGC AGGTTCTTGC CAGTTACATA 840
 AATCCCGTCA GTAGTGCAGGT AAATGGAGAA GCTCAGTCAT CTCATGAGAC TAGAGGGCAG 900
 AACAGTAATG CCCTCCCTTC TGTACTTCTC GAGCTTCTCA GTCAGTCCTG CCTCATCCCA 960
 GCCATGTCAT CTTATCTACG AAATGATTCA GTTCTGGACA TGGCAAGACA TGTGCCACTC 1020
 TATCGGGCAC TGCTGGAATT GCTTCGGGCC ATTGCTTCTT GTGCTGCCAT GGTGCCCTA 1080
 TTGTTGCCCTT TTTCTACAGA GAACGGTGAA GAGGAAGAAC AACAGTCAGA ATGTCAAAC 1140
 TCTGTTGGTA CATTGTTAGC CAAAATGAAG ACCTGTGTTG ATACCTATAC CAACCGTTA 1200
 AGATCTAAAA GGGAAAATGT TAAAACAGGA GTAAAACCAG ATGCGTCTGA TCAAGAACCA 1260
 GAAGGACTTA CTCTTTGGT ACCAGACATC CAAAAGACTG CTGAGATAGT TTATGCAGCC 1320
 ACCACCAGTT TGCAGCAAGC AAATCAGGAA AAAACTGGG TGAATACTCC AAGAAGGCAG 1380
 CTAATGAACC CCAAACCTTT GTCAGTATTA AAGTCACTTG AAGAAAAATA TGTGGCTGTT 1440
 ATGAAGAAAT TACAGTTGA TACGTTGAA ATGGTTCTG AAGATGAAGA TGGGAAATTG 1500

GGATTTAAAG TAAATTACCA CTACATGTCT CAGGTGAAAA ATGCTAATGA TCGAACAGT 1560
GCTGCCAGAG CTCGCCGCCT TGCCCAGGAA GCTGTGACGC TTTCAACCTC ACTGCCTCTG 1620
TCTTCATCCT CTAGTGTGTT TGTACGCTGT GATGAGGAGC GACTTGATAT CATGAAGGTT 1680
CTAATAACTG GTCCAGCGGA CACCCCTTAT GCAAATGGCT GCTTGAGTT TGATGTGTAT 1740
TTTCCTCAAG ATTATCCCAG TTCACCCCT CTTGTGAATC TAGAGACAAC TGGTGGTCAT 1800
AGCGTGCAGAT TCAATCCAAA CCTTTATAAT GATGGCAAGG TTTGTTAAG CATCTTAAAC 1860
ACGTGGCATG GAAGACCGAGA AGAGAAGTGG AATCCTCAGA CCTCAAGCTT TTTGCAAGTG 1920
TTGGTGTCTG TCCAGTCCCT TATATTAGTA GCTGAGCCTT ATTTTAATGA ACCGGGATAT 1980
GAACGGTCTA GAGGCACCTCC CAGTGGCACA CAGAGTTCTC GAGAATATGA TGGAAACATT 2040
CGACAAGCAA CAGTTAAGTG GGCAATGCTA GAACAAATCA GAAACCCCTTC ACCATGTTT 2100
AAAGAGGTAA TACACAAACA TTTTACTTG AAAAGAGTTG AGATAATGGC CCAATGTGAG 2160
GAGTGGATTG CGGATATCCA GCAGTACAGC AGTGATAAGC GGGTAGGCAG GACTATGTCT 2220
CACCATGCAG CAGCTCTCAA GCGTCACACT GCTCAGCTCC GCGAAGAGTT GCTGAAACTT 2280
CCCTGCCCTG AAGGCTTGGA TCCTGACACT GACGATGCC CAGAGGTGTG CAGAGCCACA 2340
ACAGGTGCTG AGGAGACTCT AATGCATGAT CAGGTTAAC CCAAGCAGCAG CAAAGAACTC 2400
CCCAGTGACT TCCAGTTATG AGCTGCATTG ATGTGGACTT CATAGACACA AAGGCTTCGA 2460
AGCACAAGCC AAATATGTCA ATATTGTAT GTAAGAAACT AATTATGTAA TAGGTAATGA 2520
AACTGAAACT ATACTATGCC CTTAAGGAGA TCCAGTTAA TTCAAGGTGA TCTTTATTT 2580
ACCTGTACAG GAGTGTAAAC TTTTTGTGC TTTTATTTT CAATTGTGAG AACCACTGAT 2640
TGGTATGTTCA AACAAATTG TGTATACAAA GAAATGGATA AATCACTGCT ATATAAGGGA 2700
AACTACCTTA GGAAAGAATG TTTACTGAAT GTTATTTTA TTTTATTTT TTTTACTAT 2760
AGAGTGAGGG GTTGTAAACA AAGAATATAT ATTGGTCGTT CTTACAACTA CTATTTAAAG 2820
TCAGCAACTT TTCACTGAAT TTGATAGATT TTATGTTGG GGGTACGAGC TTGTAAAGCT 2880
CGGGTGCCTN ATGAGTGACC 2900

(2) INFORMATION FOR SEQ ID NO: 97:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:

(A) LIBRARY: LUNGNOT14
(B) CLONE: 1510839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97 :

CCGCTGAGAT GTACGAACTT CCGGTTCTCC GGGCAGCTGC CACTGCTGTA GCTTCTGCCA 60
CCTGCCACGA CGGGGCCTCT CCCTGGCGTT TGGTCACCTC TGCTTCATTC TCCACCGCGC 120
CTATGGTCCC TCTTGGAGCC AGCGTGGCGG GCCTGGCGGC TCCCGGGTGG TGAGAGAGCG 180
GTCCGGGAAC GATGAAGGCC TCGCAGTGCT GCTGCTGTCT CAGCCACCTC TTGGCTTCCG 240
TCCTCCCTCT GCTGTTGCTG CCTGAACTAA GCAGGGCCCT GGCAGTCCTG CTGCAGGCAG 300
CCGAGGCCGC GCCAGGTCTT GGGCCTCCTG ACCCTAGACC ACGGACATTA CCGCCGCTGC 360
CACCGGGCCC TACCCCTGCC CAGCAGCCGG GCCGTGGTCT GGCTGAAGCT GCGGGGCCGC 420
GGGGCTCCGA GGGAGGCAAT GGCAGCAACC CTGTGGCCGG GCTTGAGACG GACGATCACG 480
GAGGGAAGGC CGGGGAAGGC TCGGTGGGTG GCGGCCTTGC TGTGAGCCCC AACCTGGCG 540
ACAAGCCCAC GACCCAGCCGG GCCCTGACCG TGTGATGGT GGTGAGCGGC GCGGTGCTGG 600
TGTACTTCGT GGTCAGGACG GTCAGGATGA GAAGAAGAAA CCGAAAGACT AGGAGATATG 660
GAGTTTGGA CACTAACATA GAAAATATGG AATTGACACC TTTAGAACAG GATGATGAGG 720
ATGATGACAA CACGTTGTT GATGCCAATC ATCCTCGAAG AAGAGAATGT GCCTTTGAT 780
GAAAGAACTT TATCTTCTA CAATGAAGAG TGGAAATTCT ATGTTAAGG AATAAGAAC 840
CACTATATCA ATGTTGGGG GGTATTTAAG TTACATATAT TTTAACAAACC TTTAATTGC 900
TGTGCAATA AATACCGTAT CCTTTTATTA TATCTTATA TGTATAGAAG TACTCTATTA 960
ATGGGCTCAG AGATGTTGGG GATAAAGTAT ACTGTAATAA TTTATCTGTT TGAAAATTAC 1020
TATAAAACGG TGTTTCTGA TCGGTTTTG TTTCTGCTT ACCATATGAT TGAAATTGT 1080
TTTATGTATT AATCAGTTAA TGCTAATTAT TTTGCTGAT GTCATATGTT AAAGAGCTAT 1140
AAATTCCAAC AACCAACTGG TGTGTAAAAA TAATTTAAAA TTTCTTTAC TGAAAGGTAT 1200
TTCCCATTAA TGTGGGGAAA AGAAGCCAAA TTTATTACTT TGTGTTGGGG TTTTAAAT 1260
ATTAAGAAAT GTCTAAGTTA TTGTTGCAA AACAAATAAT ATGATTAG 1310

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2272 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: SPLNNNOT04
 (B) CLONE: 1534876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98 :

CCATGCTCCA GGCATACAGA TGTGGTTCT CGGCTGCACC GGGCCAGGCT GCGGGTGTGC 60
 AGGCGTCTGC AAAGTTGTGC CATGTATCAG CACAGGCTT GAGACGTCTG GACCCTGTCC 120
 TTCCTCCCGT GAGGGGTTCT TGTCTTTCT GACTCAGGTG ACTTTCAGC CCTTCCAATT 180
 CCCCTTTT TCTGCCCTCC CCTCCAACTC AGCCAACCCA GGTGTGGCA GTCAGGGAGG 240
 GAGGGAGTGT CCCACCACGT TCTCAGGGCA GCCCTTGACT CCTAAGCCCC TTCCTCCTTC 300
 CATTCTGCAT CCCCTCCCCA TCCAACCTAA ATGCCACAG CTGGGCTGA GCTGTATTCC 360
 TGTGGAGGGA CCTCTGCCGT GCCTCTCTGA GGTCAAGGCTG TGCTGTGTGA TGGCAGGCT 420
 TTGCCCCAGC CCACCCCTGG CAAGGTGCAC TTGTTTCTG GTTGTACAA GGTGTCTGG 480
 GGGCCCGTCG CTTCCCTGCC AGTGAGGAGT GACTTCTCCC TCTCTCCAG TCCTGTAGGG 540
 GAGACAAAAC CAGATTGGGG GGCCCAAGGG GAGCATGGAA AAGGCCGGCT CCCCTGTCTT 600
 TCCTTGGCTG TCAGAGTCAG GGTAACACAC ACCAAGAGTG GAGTGCAGGCC AGCAAGTTG 660
 AGACCTGCC CCCCCTCTCG CAGCTCTGCT CTGTGTCTC AGGAAGTCAC AGAGTCTACT 720
 GAGGCAAGGA GAGGGTGATT CTTCCCCAA ATCCCTTCTT CCCTGGTTCC CAAACCAAAG 780
 ACAGCCTGCA GCCCTTCTG CATGGGTC TCTGTTGACA GGCTTCCAG ATCCCTGAGT 840
 CTCTCTTCC TTCCCTCTCG ATCTTAGTT GTCCACGGTC AATTCACTGC TTCCATTGGG 900
 GGACAGTCCC CTCCGGGATG ACCTGATTCA CCTCCAGCCC AGGAATGGA ATCTAGAGGA 960
 ATACGTGGGG TGGGTCTGGA CAAGGAGCGG CAGGAATCAC CACCCATCTC CAGCTGTGGA 1020
 GCCCTGTGGA GGGGAAGGGG AAGCTTGGGG TTCAGAGGGAA ACTCTTCCAG GAGAGGGGTG 1080
 CCCAGCGGAG GTAAAGATGA TAGAGGGTTG TGGGGGGTCT CTAGTTGAAT GTTTGGGCC 1140
 ATGACTTTGG AACATGGCTG GCAGCTTCCA GCAGAAGTCA CGCTCCCCAT CCCCCAGGGG 1200
 ACATAGGACC TTTTCCTGC TTCCCTGGTCA CTTCAAAGA ACTATTGCG CAATCTGTGG 1260
 GTCTGTGGAT TCACGGGCT TTCTGTGTGG GTGCTGCAGT TGCTTTGTC TGCAGCAGCA 1320
 GGACACATCT TTCCCTTAC TCAGCCCTT ATGGCCCATG GGGAACTCCG TGGCTCAGGG 1380
 AGAGCTGAAC TCCAGGGGTG TGACCTGGGA CAGGTGGGCC TGAGGTGCC AGCTCAGGGC 1440
 AGCCAGGTGG CTCATGGGCT GTAGTGAGCC AGCTCCCTGG GGGAAAAGGC TGTGGGCCGT 1500
 TAGGACCATC CTCCAGGACA GGTGACCTCT ATGAGGTACAC CTACGGCTGT GGCGTGCAG 1560
 GCCTCCTTCC AGCCCAGAGT GGCCCAGTAG AGCAAGGCAG ACAGTGACCT CCACCCCCGC 1620
 AGCCCTTTA AAAGGCCAGT ACTCTTGGGG GTGGGGGGAG GTTTAGAAA GCATTTGCC 1680

ATCTGCCTT CTTCCCCCA GCCCCCACCC GCTTGATG TAGAGACCCG TGGGCACTT 1740
 TCCTTTGTG GTGGGGGGTG CGGAGGAGGT ACCCCCACCC CTGGCACAGC CGCCTGGAAT 1800
 GCAGGACTGT CACTGCTGTT CGGGTGATGA CCTCGTTGCC AAGCTCCTCC TGTCCCCTG 1860
 TTCTGGGGC AGGCGCTGTG CTTCTGTGAG GTGGTTAGC TTTGCTTTC GAAGTGGCCA 1920
 GCTGCGGCCA CCAGGTCTCA GCACAAGAGC GCTTCCTTG CACAGAATGA GCTTCGAGCT 1980
 TTGTTCAGAC TAAATGAATG TATCTGGGAG GGGTCGGGG CACGAGTTGA TTCCAAGCAC 2040
 ATGCCTTGC TGAGTGTGTG TGTGCTGGGA GAGTCAGAGT GGATGTAGAG CGCGGTTTA 2100
 TTTTGTACT GACATTGGTA AGAGACTGTA TAGCATCTAT TTATTTAGAT GATTATCTG 2160
 GTAAATGAGG CAAAAAAATT ATTAAAAATA CATTAAAGAT GATTTAAAAA AAAGACCAAA 2220
 AACCAAGAA ACCCAAAGCC CAAGAATGCG CGTAGCATCC AAAAAAAA GG 2272

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1060 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: SPLNNOT04
 - (B) CLONE: 1559131
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99 :

GTCAACTTAG CGAGCGAAC AGGCTGCCGC TGAGGAGCTG GAGCTGGTGG GGACTGGGCC 60
 GCAATGGACA AGCTGAAGAA GGTGCTGAGC GGGCAGGACA CGGAGGACCG GAGCGGCCTG 120
 TCCGAGGTTG TTGAGGCATC TTCATTAAGC TGGAGTACCA GGATAAAAGG CTTCATTGCG 180
 TGTTTGCTA TAGGAATTCT CTGCTCACTG CTGGGTACTG TTCTGCTGTG GGTGCCAGG 240
 AAGGGACTAC ACCTCTTCGC AGTGTGTTAT ACCTTTGGTA ATATCGCATC AATTGGGAGT 300
 ACCATCTTCC TCATGGGACC AGTGAAACAG CTGAAGCGAA TGTGAGGCC TACTCGTTG 360
 ATTGCAACTA TCATGGTGCT GTTGTGTTT GCACTTACCC TGTGTTCTGC CTTTGGTGG 420
 CATAACAAGG GACTTGCACT TATCTTCTGC ATTTGCACT CTTGGCATT GACGTGGTAC 480
 AGCCTTCCT TCATACCATT TGCAAGGGAT GCTGTGAAGA AGTGTGTTGC CGTGTGTCTT 540
 GCATAATTCA TGGCCAGTT TATGAAGCTT TGGAAAGGCAC TATGGACAGA AGCTGGTGG 600
 CAGTTTGTA ACTATCTTCG AAACCTCTGT CTTACAGACA TGTGCCTTT ATCTTGCAGC 660
 AATGTGTTGC TTGTGATTG AACATTTGAG GGTTACTTT GGAAGCAACA ATACATTCTC 720

GAACCTGAAT GTCAGTAGCA CAGGATGAGA AGTGGGTTCT GTATCTTGTG GAGTGGAATC 780
TTCCTCATGT ACCTGTTCC TCTCTGGATG TTGTCCCACT GAATTCCCAT GAATACAAAC 840
CTATTCAGCA ACAGCACATA AGCCTTGGGT GCAAGTGATT CCCAGGTGGC AAAAGGCAGC 900
CCCATCAGAG ATCACGGGAG CAACAGTAAG GGACAGAGTT TTGGGGTCCA CTTGTCCCTC 960
AGCATGGAAG CCATCACCGT GGTCTGCAT AGAGTGAGTC TGCTTCTACT CTGGCATCTG 1020
AGAACAAAGTG ACTCTGCTTT AGACAAGCCC CTGGAGAGGG 1060

(2) INFORMATION FOR SEQ ID NO: 100:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 543 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: BLADNOT03
(B) CLONE: 1601473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100 :

GCTCACAGTA GCCCGGCGGC CAGGGCAATC CGACCACATT TCACTCTCAC CGCTGTAGGA 60
ATCCAGATGC AGGCCAAGTA CAGCAGCACA AGGGACATGC TGGATGATGA TGGGGACACC 120
ACCATGAGCC TGCATTCTCA AGCCTCTGCC ACAACTCGGC ATCCAGAGCC CCGGCGCACA 180
GAGCACAGGG CTCCCTCTTC AACGTGGCGA CCAGTGGCCC TGACCCCTGCT GACTTTGTGC 240
TTGGTGCTGC TGATAGGGCT GGCAAGCCTG GGGCTTTGT GTAAGTCTGC GCTCTGACCT 300
GGGGGAGGAT CCTGGTTCCA AGTTTTCAAG TACTACCAGC TCTCCAATAC TGGTCAAGAC 360
ACCATTCTC AAATGGAAGA AAGATTAGGA AATACGTCCC AAGAGTTGCA ATCTCTTCAA 420
GTCCAGAATA TAAAGCTTGC AGGAAGTCTG CAGCATGTGG CTGAAAAACT CTGTCGTGAG 480
CTGTATAACA AAGCTGGAGC ACACAGGTGC AGCCCTTGT AAGAACAAATG GAAATGGCAT 540
GGA 543

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2281 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: BRAITUT12
(B) CLONE: 1615809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101 :

AGCTGGCTCA CCTTCCAGAT TCACCTGCAG GAGCTGCTGC AGTACAAGAG GCAGAATCCA 60
GCTCAGTTCT CGCTTCGAGT CTGCTCTGGC TGTGCTGTGT TGGCTGTGTT GGGACACTAT 120
GTTCCAGGGA TTATGATTTC CTACATTGTC TTGTTGAGTA TCCTGCTGTG GCCCCTGGTG 180
GTTTATCATG AGCTGATCCA GAGGATGTAC ACTCGCCTGG AGCCCTGCT CATGCAGCTG 240
GACTACAGCA TGAAGGCAGA AGCCAATGCC CTGCATCACA AACACGACAA GAGGAAGCGT 300
CAGGGGAAGA ATGCACCCCC AGGAGGTGAT GAGCCACTGG CAGAGACAGA GAGTGAAAGC 360
GAGGCAGAGC TGGCTGGCTT CTCCCCAGTG GTGGATGTGA AGAAAACAGC ATTGGCCTTG 420
GCCATTACAG ACTCAGAGCT GTCAGATGAG GAGGCTTCTA TCTTGGAGAG TGGTGGCTTC 480
TCCGTATCCC GGGCCACAAC TCCGCAGCTG ACTGATGTCT CCGAGGATTG GGACCAGCAG 540
AGCCTGCCAA GTGAACCAGA GGAGACCCTA AGCCGGGACC TAGGGGAGGG AGAGGAGGGA 600
GAGCTGGCCC CTCCCGAAGA CCTACTAGGC CGTCCTCAAG CTCTGTCAAG GCAAGCCCTG 660
GACTCGGAGG AAGAGGAAGA GGATGTGGCA GCTAAGGAAA CCTTGTGCG GCTCTCATCC 720
CCCCCTCCACT TTGTGAACAC GCACTTCAAT GGGCAGGGT CCCCCCAAGA TGGAGTGAAA 780
TGCTCCCCTG GAGGACCACTG GGAGACACTG AGCCCCGAGA CAGTGAGTGG TGGCCTCACT 840
GCTCTGCCCG GCACCCCTGTC ACCTCCACTT TGCCTTGTG GAAGTGACCC AGCCCCCTCC 900
CCTTCCATTC TCCCACCTGT TCCCCAGGAC TCACCCCCAGC CCCTGCCTGC CCCTGAGGAA 960
GAAGAGGCAC TCACCACTGA GGACTTGAG TTGCTGGATC AGGGGGAGCT GGAGCAGCTG 1020
AATGCAGAGC TGGGCTTGGA GCCAGAGACA CCGCCAAAAC CCCCTGATGC TCCACCCCTG 1080
GGGCCCGACA TCCATTCTCT GGTACAGTCA GACCAAGAAG CTCAGGCCGT GGCAGAGCCA 1140
TGAGCCAGCC GTTGAGGAAG GAGCTGCAGG CACAGTAGGG CTTCTGGCT AGGAGTGTG 1200
CTGTTTCCTC CTTTGCCTAC CACTCTGGGG TGGGGCAGTG TGTGGGAAG CTGGCTGTCG 1260
GATGGTAGCT ATTCCACCCCT CTGCCTGCCT GCCTGCCTGC TGTCTGGGC ATGGTGCAGT 1320
ACCTGTGCCT AGGATTGGTT TTAAATTGT AAATAATTTC CCATTTGGGT TAGTGGATGT 1380
GAACAGGGCT AGGGAAGTCC TTCCCACAGC CTGCGCTTGC CTCCCTGCCT CATCTCTATT 1440
CTCATTCCAC TATGCCCAA GCCCTGGTGG TCTGGCCCTT TCTTTTCCT CCTATCCTCA 1500
GGGACCTGTG CTGCTCTGCC CTCATGTCCC ACTTGGTTGT TTAGTTGAGG CACTTTATAA 1560
TTTTTCTCTT GTCTTGTGTT CCTTCTGCT TTATTTCCCT GCTGTGCCT GTCCTTAGCA 1620
GCTCAACCCC ATCCTTGCC AGCTCCTCCT ATCCCGTGGG CACTGCCAA GCTTTAGGGA 1680

PF-0459 US

GGCTCCTGGT CTGGGAAGTA AAGAGTAAAC CTGGGGCAGT GGGTCAGGCC AGTAGTTACA 1740
CTCTTAGGTC ACTGTAGTCT GTGTAACCTT CACTGCATCC TTGCCCCATT CAGCCCGGCC 1800
TTTCATGATG CAGGAGAGCA GGGATCCCGC AGTACATGGC GCCAGCACTG GAGTTGGTGA 1860
GCATGTGCTC TCTCTTGAGA TTAGGAGCTT CCTTACTGCT CCTCTGGGTG ATCCAAGTGT 1920
AGTGGGACCC CCTACTAGGG TCAGGAAGTG GACACTAACAA TCTGTGCAGG TGTTGACTTG 1980
AAAAATAAAG TGTTGATTGG CTAGAACTGC TGCCTCCCTG ACTGTGAGCT GCCTTCCACA 2040
CCCTGCACTG CACTGTGTT CTCCTCACC CTTAACCTGC TTCACTCCAG TCTGTTCTGG 2100
CTGTTTATTA CCTTGTTGCA AACAGGGCC GAAGCAAGGA TTACCTTGAC AACCTAGCT 2160
TCTCCTTAGC CATCTTCCTT GACAGTGTGA TCTGTTAGT GAGATTAGC ATGTGTGAAT 2220
AAAGTATATG CAGGAGGAAA TTGCTTGTC TTCCAATCG GTAGAAATTC GAGACCTAGC 2280
C 2281

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 992 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: COLNNOT19
(B) CLONE: 1634813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102 :

GACAGCTTGG CCTACAGCCC GGCGGGCATC AGCTCCCTTG ACCCAGTGG A TATCGGTGGC 60
CCCGTTATTG GTCCAGGTGC CCAGGGAGGA GGACCCGCCT GCAGCATGAA CCTGTGGCTC 120
CTGGCCTGCC TGGTGGCCGG CTTCCTGGGA GCCTGGGCC CCGCTGTCCA CGCCCAAGGT 180
GTCTTGAGG ACTGCTGCCT GGCCTACAC TACCCATTG GGTGGCTGT GCTCCGGCGC 240
GCCTGGACTT ACCGGATCCA GGAGGTGAGC GGGAGCTGCA ATCTGCCTGC TGCGATATT 300
TACCTCCCCA AGAGACACAG GAAGGTGTGT GGGAAACCCA AAAGCAGGGA GGTGCAGAGA 360
GCCATGAAGC TCCTGGATGC TCGAAATAAG GTTTTGCAA AGCTCCGCCA CAACACGCAG 420
ACCTTCCAAG CAGGCCCTCA TGCTGTAAAG AAGTTGAGTT CTGGAAACTC CAAGTTATCA 480
TCATCCAAGT TTAGCAATCC CATCAGCAGC AGCAAGAGGA ATGTCTCCCT CCTGATATCA 540
GCTAATTCAAG GACTGTGAGC CGGCTCATTT CTGGGCTCCA TCGGCACAGG AGGGGCCGG 600
TCTTCTCCG ATAAAACCGT CGCCCTACAG ACCCAGCTGT CCCCACGCCT CTGTCTTTG 660

GGTCAAGTCT TAATCCCTGC ACCTGAGTTG GTCTCCCTC TGCACCCCCA CCACCTCCTG 720
 CCCGTCTGGC AACTGGAAAG AGGGAGTTGG CCTGATTTA AGCCTTTGC CGCTCCGGGG 780
 ACCAGCAGCA ATCCTGGGCA GCCAGTGGCT CTTGTAGAGA AGACTTAGGA TACCTCTCTC 840
 ACTTTCTGTT TCTTGCCGTC CACCCCGGGC CATGCCAGTG TGTCCCTCTG GGTCCCTCCA 900
 AAACCTCTGGT CAGTTCAAGG ATGCCCTCC CAGGCTATGC TTTCTATAA CTTTTAAATA 960
 AACCTTGGGG GTTGATGGAG TCAAAAAAAA AA 992

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1554 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: UTRSNOT06
 - (B) CLONE: 1638407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103 :

TCGCCCAGGA GTCATCGGAC GCCAGAACCT GTGTCTCCAG AACGCTATAG CTATGGCACC 60
 TCCAGCTCTT CAAAGAGGAC AGAGGGTAGC TGCCGTCGCC GTCGGCAGTC AAGCAGTTCT 120
 GCAAATTCTC AGCAGGGTCA GTGGGAGACA GGCTCCCCCC CAACCAAGCG GCAGCGGGGG 180
 AGTCGGGGCC GGCCCAGTGG TGGTGCCAGA CGGCGGGCGGA GAGGGGCCAGG AGCCGCACCC 240
 CAGCAGCAGT CAGAGCCCCGC CAGACCTTCC TCTGAAGGCA GGTGACACTG TGATGGGGAA 300
 ACAGGCTCAG AGAGACATCC GGCTCCGGGT TCGAGCAGAG TACTGCGAGC ATGGGCCAGC 360
 CTTGGAGCAG GGCAGTGGCAT CCCGGCGGCC CCAGGCGCTG GCGCGGCAGC TGGACGTGTT 420
 TGGCAGGCC ACCGCAGTGC TGCGCTCAAG GGACCTGGGC TCTGTGGTT GTGACATCAA 480
 GTTCTCAGAG CTCTCCTATC TGGACGCCTT CTGGGGCGAC TACCTGAGTG GCGCCCTGCT 540
 GCAGGCCCTG CGGGCGTGT TCCTGACTGA GGCCCTGCGA GAGGCTGTGG GCCGGGAGGC 600
 TGTTCGCCTG CTGGTCAGTG TGGATGAGGC TGACTATGAG GCTGGCCGGC GCCGCCTGTT 660
 GCTGATGGCG GAGGAAGGGG GGCGGGCGCC GACAGAGGCC TCCTGATCCA GGACTGGCAG 720
 GATTGATCCC ACCTCCAAGT CTCCGGGCCA CCTTCTCCTG GGAGGACGAC CATCTCTACC 780
 CCTAGAGGAC TGTCACTCTA GCATCTTGA GGACTGCGAC AGGACCGGGA CAGCAGGCC 840
 CTTGACAGCC CCTCCCACAG GATGTGGCT CTGAGGCCTA AACCATTTCC AGCTGAGTTT 900
 CCTTCCCAGA CTCCTCCTAC CCCCAGGTGT GCCCCCTTAG CCTCCGGAGG CGGGGGCTGG 960

PF-0459 US

GCCTGTATCT CAGAAGGGAG GGGCACAGCT ACACACTCAC CAAAGGCCCT CCTGCACATT 1020
GTATCTCTGA TCTTGGGCTG TCTGCAGTGT CACAGGTGCA CACACTCGCT CATGCTCACA 1080
CTGCCCCCTGC TGAGATCTTC CCTGGGCCTC TGCCCTGGCC TGCTTCCAG CACACACTTC 1140
TTTGGCCTAA GGGCTTCTCT CTCAGGACCT CTAATTGAC CACAACCAAC CTGGGCTTCA 1200
GCCACATCAG TGGGCACTGG AGCTGGGTG CACATGGGC CTGCTCACCT TGCCCACACA 1260
TCTCCAGCCA GCCAGGGCCC TGCCCAGCTT CAATTTACAG ACCTGACTCT CCTCACCTTC 1320
CCCCCTGCTG TCCAGAGCTG AACATAGACT TGCACTTGGA TGTCACCTGG AGTGTACAT 1380
GGGAGTGTAA TGGCAGCAGC ATACCAAGGC CTACTGTTGC ACATGGGCC AAAACCAGTA 1440
AACAGCCACC TTCTGGAAA GGGAAATGCAA AGGCTTGGA GGTGATGGAA AAGACCTTT 1500
ACAAATGATA CCAATTAAC TGCCCTGGAA AGGGCATAGG TGGGAAAAAA AAAA 1554

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1802 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: PROSTUT08
(B) CLONE: 1653112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104 :

GTCGCCGGGC TTGCGATGAA CTTCCGGCTG TCAAGCTCCC GGCCGGGCTG ACTCAAGCGG 60
AGGCGCGCGG AACAGTCGCC GAGGCGATTC CCGCCCAGGC TCCTGTAACC GCCAGGCAGC 120
GGCCCCGCCA TGTCCCAGCC CCGGACCCCA GAGCAGGCAC TGGATACACC GGGGGACTGC 180
CCCCCAGGCA GGAGAGACGA GGACGCTGGG GAGGGGATCC AGTGTCCCA ACGCATGCTC 240
AGCTTCAGTG ACGCCCTGCT GTCCATCATC GCCACCGTCA TGATCCTGCC TGTGACCCAC 300
ACGGAGATCT CCCCAGAACCA GCAGTTCGAC AGAAAGTGTAC AGAGGCTTCT GGCAACACGG 360
ATTGCCGTCT ACCTGATGAC CTTTCTCATC GTGACAGTGG CCTGGGCAGC ACACACAAGG 420
TTGTTCCAAG TTGTTGGAA AACAGACGAC ACACCTGCC TGCTAACCT GGCCTGCATG 480
ATGACCATCA CCTTCCTGCC TTACACGTT TCGTTAATGG TGACCTTCCC TGATGTGCCT 540
CTGGGCATCT TCTTGTCTG TGTGTGTGTG ATCGCCATCG GGGTCGTGCA GGCACGTGATT 600
GTGGGGTACG CATTCCACTT CCCGCACCTG CTGAGCCCGC AGATCCAGCG CTCTGCCAC 660
AGGGCTCTGT ACCGACGACA CGTCCTGGC ATCGTCCTCC AAGGCCCGC CCTGTGCTTT 720

PF-0459 US

GCAGCGGCCA TCTTCTCTCT CTTCTTGTC CCCTTGTCTT ACCTGCTGAT GGTGACTGTC 780
ATCCTCCTCC CCTATGTCAG CAAGGTCACC GGCTGGTGCA GAGACAGGCT CCTGGGCCAC 840
AGGGAGCCCT CGGCTCACCC AGTGGAAAGTC TTCTCGTTG ACCTCCACGA GCCACTCAGC 900
AAGGAGCGCG TGGAAGCCTT CAGCGACGGA GTCTACGCCA TCGTGGCCAC GCTTCTCATC 960
CTGGACATCT GCGAAGACAA CGTCCCAGAC CCCAAGGATG TGAAGGAGAG GTTCAGCGGC 1020
AGCCTCGTGG CGGCCCTGAG TGCGACCGGG CGCGCCTTCC TGGCGTACTT CGGCTCCTTC 1080
GCCACAGTGG GACTGCTGTG GTTCGCCCAC CACTCACTCT TCCTGCATGT GCGCAAGGCC 1140
ACGCGGGCCA TGGGGCTGCT GAACACGCTC TCGCTGGCCT TCGTGGGTGG CCTCCCACTA 1200
GCCTACCAGC AGACCTCGGC CTTCGCCCCG CAGCCCCGCG ATGAGCTGGA GCGCGTGCCT 1260
GTCAGCTGCA CCATCATCTT CCTGGCCAGC ATCTTCCAGC TGGCCATGTG GACCACGGCG 1320
CTGCTGCACC AGGCGGAGAC GCTGCAGCCC TCGGTGTGGT TTGGCGGCCG GGAGCATGTG 1380
CTCATGTTCG CCAAGCTGGC GCTGTACCCC TGTGCCAGCC TGCTGGCCTT CGCCTCCACC 1440
TGCCTGCTGA GCAGGTTCAAG TGTGGGCATC TTCCACCTCA TGCAGATCGC CGTGCCCTGC 1500
GCCTTCCTGT TGCTGCGCCT GCTCGTGGC CTGGCCCTGG CCACCCCTGCG GGTCCCTGCC 1560
GGCCTCGCCC GGCCCCAACCA CCCCCCGCCA GCCCCCCACGG GCCAGGACGA CCCACAGTCC 1620
CAGCTCCTCC CTGCCCCCTG CTAGCAGCCA CAGAGCCCAC TCCCAGCCGT CCTCACCAGA 1680
GATGGACCAG GGAGGACAGG ATGCTGGCA GGGGAAGCCA AGTCACGGC AGGCCGCAGT 1740
GGTTCTTGCCTGGCCTT TTATTTCAT TGTGAAATAT CATGCTCTTA TTTCAAGTCCT 1800
CA 1802

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1395 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: BRSTNOT09
(B) CLONE: 1664634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105 :

GTACCTCGGC TTATTCATA AACAGGTACT GAAGGAAAGCA GAGGCATGTG GAGGACTTCC 60
CCACCTCGTG CAGCTATTTG GGCGTGGCA TCTGAAATTT CTTATTCAG AGTCACCCCT 120
TTGATGACCT TGGCAGTGAA CTGCAGTCAT CTGTTAGGC CTTTCCATGG CCCACGTCAA 180

PF-0459 US

TGCCGGTATT TCTGTTGTT GCACATTGA TTTCCTGTT GTTGGCATT AGAAGGCCCT 240
CGAGCCGCAC TGAGGGACTG AGCCTGGTGT ATATGGCAGC AAGACTGGAT GGTGGCTTG 300
CAGCAGTCTC CAGAGCATTG CATGAGATCC GGGCTCGAAA TCCAGCATT CAGCCACAAA 360
CTTGATGGA CTTGGCTCA GGTACTGGTT CTGTCACCTG GGCTGCTCAC AGTATTTGGG 420
GCCAGAGCCT ACGTGAATAT ATGTGTGTGG ACAGATCAGC TGCCATGTTG GTTTGGCAG 480
AAAAACTACT GACAGGTGGT TCAGAATCTG GGGAGCCTTA TATTCCAGGT GTCTTTTCA 540
GACAGTTCT ACCTGTATCA CCCAAGGTGC AGTTTGATGT AGTAGTGTCA GCTTTTCCT 600
TAAGTGACCA GCTACTGACA TTTATACTTT CGTGTAAATTG AAGTCTTCTG CATATTTCC 660
CCTTTGTGA ACAGGTACTG GTGGAGAATG GAACAAAAGC TGGGCACAGC CTTCTCATGG 720
ATGCCAGGGA TCTGGCCTT AAGGGAAAAG AGAAGTCACC TTTGGACCCCT CGACCTGGTT 780
TTGTCTTGC CCCGTGTCCC CATGAACCTCC CTTGTCCCCA GTTGACCAAC CTGGCCTGTA 840
GCTTCTCACA GGCGTACCAT CCCATCCCC TCAGCTGGAA CAAGAAACCA AAGGAAGAAA 900
AGTTCTCTAT GGTGATCCTT GCTCGGGGGT CTCCAGAGGA GGTCATCGC TGGCCCCGTA 960
TCACTCAGCC TGTCCCTAAA CGGCCTCGCC ATGTGCATTG TCACTTGTGC TGTCCAGATG 1020
GGCACATGCA GCATGCTGTG CTCACAGCCC GCCGGCACGG CAGGTATGGG GGGTGTGACC 1080
AAAATCAGTG GGATGTGGCA GGAAGCTGCA GCCCACGCCA GCATCTGTT CCACAGGGAT 1140
TTGTATCGTT GTGCCCGTGT CAGCTCCTGG GGAGATCTT TACCTGTGCT TACTCCGTCT 1200
GCGTTTCCTC CATCTACGGC TCAGGATCCC TCTGAGAGTT GATGAGGATG TGTAACAAGT 1260
ATTTTCTTCT ATCGTGCCTG CCAGGGCTGA AGCTGCCTGG TATCCAGGAG GGGAAATGCTG 1320
GTATCCCCAT ATGTCTGTGT TTGTTGAGA TTTTAATAA TAAATAATAA ATTTTGAAAG 1380
AATGGAAAAA AAAAAA 1395

(2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1635 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: PROSTUT10
 - (B) CLONE: 1690990
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106 :

CCCTCTTCCT TTTGCGCACG GAAGAACAAA TCACACAAT CACACACCAG GACTGAATCC 60

ATCAGCAGAT ACTGCCCTGT GGGAAAGGCA GAGGAAAGAG AAGACAGACG GACTGACAGA 120
 CACCAACAGAG GAACAGGGGA GTTAGCCTGG GACCAATGGA GGAGAAGTAC GAACCTGGG 180
 AAAAAGACGT GTCAGATGAG AAAGTTCCGG AGAGTCCGAT GTCTCATCGC AGGTGTTACA 240
 TCATCAGGGT TTGCCATTGG AATACTGAGT GGAGATGGGA AAGAGAAAAG TTAAGGGCTG 300
 AAATGGGAGG GGAATGGGAA GAAAAAAATGA GAGACAAGAG GGAAATAAGA AAAAACAAAG 360
 AGAGCACAAA GACCAGTTA GGAGAAAGGA CCAATGGGG AAGTGGCAGA GTGGCGAGGT 420
 AGGTGAAGGA CTGAGGCACA GCGTCCTGTT GTGGAGGGAG GAAAGGCAAG CGTTCCGAGG 480
 TGGTAAAAG GAAGGCCTGC TAGGCACGGT GGGGATGAAC GAGGATGCCA TGAGTCACAC 540
 AAAAGACAGT GCTGGTGAGG CCCAGCCACA GGAGCCTCAG ATAACTTGGT AAAGGCATGT 600
 CTCCCATTG GGAACGTGATG TTCCTAAGAT CCGCACTGAC GCTGCTCAGC CGGTCCATCA 660
 CACAGCAAAG GCGTGAGGAA GGGTCACTGC CCAGCTGGAC TCCAGGGTGG TCCACGCATG 720
 ACAGTCACAC CGAACCTTCA TGAGGATGTG AACTGTTGGC TCCAATTAC CATTCCCAGC 780
 AATTCCACTC AGATATTTGT ATACTAATGT TCACAGCAGC GTGAACCTCA CAGCAGGTGG 840
 AGTAATGTT CATTGTGTGC ATATGCCACA TTTGTTTAT CCATTCTAC GTTGATGCAC 900
 ATTCGGTTG TTCCCACCTT TGGGCTATTA TTAATAATGC TGCTGTGAAC ATTCCAAGA 960
 GAAATAGGAA GACGGCTTTG CTAAGAACTA AAAAAGGGAT GGACAACAAG GGCATATACC 1020
 CAGGGGCAGT GTTCTATCAT GACAGCTTTA CTGAGAGCAG AGTAGTTCTG CTCAGAATCA 1080
 GAACACTTGT TCCCTATAGC CCCCCTGATT GCCCCACAAAC CACCACCGCA TACTCCCCTT 1140
 TTCCCAACCA TGGGCAGCAG ATTGAGCTAT TAACAGAAAGT GTCCTTCGC TGGATTTCTC 1200
 AACCCCTTCC TCATCGTCCA CATAGAGAAA CAGTAACAGA TTGCTACTCA CCCAACACCC 1260
 AGGTCAAGTC CAATGCAGGT AGGAATAACA GCAAATCCTT CAATTCTTG ATTCTGCTCT 1320
 TAAAAATCTT AACAGAGGCT TCCAGGTTCT GAAAATATTT TCTGCATAAA CGTGTGACAC 1380
 TCCATCACGA AACTCCCTT GGTTATCTGC TTAAACTTAT CGCAAATGTC TGGAACGCTG 1440
 GTGGCTTCCA AAATCAACTC CTGGTGCTGC TTAATTAAGG TCAGGGCCAC CCGGAAGATA 1500
 ATCTTCGAGC CTTCGTTAAA CAAACAGTCC CAGATCCGAA GCACTGTCTC CACGGGCAAG 1560
 ATGTCCACAA ACAGGCAGAT GAACCAGCGG GACACCAGCA GCGTCCACAG CACACCGAGA 1620
 CGCTCCATCA GGGGG

1635

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1485 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: DUODNOT02
 (B) CLONE: 1704050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107 :

TTTTGGTCC CGNCNAAAGN CCNAAAACCC GGNACCCGGG AAGCCNCCCC AANNCNAAN 60
 TTCCCAGTTN GAANCCGAA GGNAAAACCC CGGAAAAGNA NNCNGCCCN AAANTTCNCG 120
 GGCNAAAACC CGGCCNTTT TTCCCCCCCCG GGCGGCCGTT TTGGGCCCCN GANTTTCCAT 180
 TTAAANTNCC NAGNCTTGGG CAACCTAACCC AGGNTTTCC CCCAANCTGG AAAAAGCCGG 240
 GCCAAGTTGA GCCGCACCCG CCCCAGAAGT TCAAGGGCCC CGGGCCTCCT GCGCTCCTGC 300
 CGCCGGGACC CTCGACCTCC TCAGAGCAGC CGGCTGCCGC CCCGGGAAGA TGGCGAGGAG 360
 GAGCCGCCAC CGCCTCCTCC TGCTGCTGCT GCGCTACCTG GTGGTCGCCCG TGGGCTATCA 420
 TAAGGCCTAT GGGTTTCTG CCCCAAAAGA CCAACAAAGTA GTCACACAGCAG TAGAGTACCA 480
 AGAGGCTATT TTAGCCTGCA AAACCCAAA GAAGACTGTT TCCTCCAGAT TAGAGTGGAA 540
 GAAACTGGGT CGGAGTGTCT CCTTGCTCTA CTATCAACAG ACTCTCAAG GTGATTTAA 600
 AAATCGAGCT GAGATGATAG ATTTCAATAT CCGGATCAA AATGTGACAA GAAAGTGATGC 660
 GGGGAAATAT CGTTGTGAAG TTAGTGCCCC ATCTGAGCAA GGCCAAAACC TGGAAGAGGA 720
 TACAGTCACT CTGGAAAGTAT TAGTGGCTCC AGCAGTTCCA TCATGTGAAG TACCCCTCTTC 780
 TGCTCTGAGT GGAAGTGTGG TAGAGCTACG ATGTCAAGAC AAAGAAGGGA ATCCAGCTCC 840
 TGAATACACA TGGTTAAGG ATGGCATCCG TTTGCTAGAA AATCCCAGAC TTGGCTCCCA 900
 AAGCACCAAC AGCTCATACA CAATGAATAC AAAAAGTGGAA ACTCTGCAAT TTAATACTGT 960
 TTCCAAACTG GACACTGGAG AATATTCTG TGAAGCCCGC AATTCTGTTG GATATCGCAG 1020
 GTGTCCTGGG AAACGAATGC AAGTAGATGA TCTCAACATA AGTGGCATCA TAGCAGCCGT 1080
 AGTAGTTGTG GCCTTAGTGA TTTCCGTTG TGGCCTGGT GTATGCTATG CTCAGAGGAA 1140
 AGGCTACTTT TCAAAAGAAA CCTCCTCCA GAAGAGTAAT TCTTCATCTA AAGCCACGAC 1200
 AATGAGTGAA AATGATTTCA AGCACACAAA ATCCTTTATA ATTTAAAGAC TCCACTTTAG 1260
 AGATAACACCA AAGCCACCGT TGTTACACAA GTTATTAAAC TATTATAAAA CTCTGCTTTG 1320
 TCCGACATTG GCAAAGAGGT ACACGAGGAA ATGGAATTGG TATTCATTT TAATTTCAT 1380
 GACTACTAAC TCACCTGAAC TTGCTATTTT AAACAAATAG TTCTGTCGAC ACCTAAAATA 1440
 TAATCTGGCT TCTTGTGTCT GGACTAAGTT AAAAGAATTA AAATA 1485

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 810 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: PROSNOT16
(B) CLONE: 1711840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108 :

CGAGTGAGCG CGCGGCGGCC CCTGGTCCGC CCGGCCGCGG CCGATCTAGG GGCTGGGGC 60
TGGAGGCGGG GGTGGGGGTC TGAGCTGCGT CCTGGGCTCG AGGCGTCCCC CGGGGAGTCG 120
CCTCTTAGCG GTGCGTCCGG GCTAGCGCG AGGGGCCGCC CCAAGTCTTC CCACCGCCGC 180
CACCTTAGCA GCCCGACTTG GGGCCTGGAA AGTGGAGCAC GCGGAGGTGG GAGGGCCCTG 240
CACGCGGCCCG CCGGTGGGA AGGGGACGGG CCAGGGATTG AGACTCGGGC TCTCCCTCA 300
GGATGCAGCA CCGAGGCTTC CTCCTCCTCA CCCTCCTCGC CCTGCTGGCG CTCACCTCCG 360
CGGTCGCCAA AAAGCAAGAT AAGGTGAAGA AGGGCGGCCCG GGGGAGCGAG TGCGCTGAGT 420
GGGCCTGGGG GCCCTGCACC CCCAGCAGCA AAGGATTG GGCAGTGGGT TTTCCGCGAG 480
GGCCACCTTG GGGGGGCCCA AGAACCAAC CGGCAGTCCT GGTTGAAAGG GTTGCCTCTG 540
GAAAGTTGGA AAGAAAGGAG TTTTGGGCAC CCGGACTTTG GAAAGTTGGC CAAATTTTT 600
GGAAGAAAAC TTGGCGGGTC TGCCGGTCCG TTAAATGGGG GAGGGGACAA AAGAATTGAA 660
AGCCGAAAAA ATGCTTCTC CGCCGCCAAG AGAGGTCGAA CCCGCGTCTG GCAAGAAGAG 720
AAAAGGGCGC GCCCACACTG TTAACAAACAA TATGGCGCCT GAACAGTTGG TGGCACCACA 780
GGGGGAGGGGA GACACATACT TGCGCGCGGT 810

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1064 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109 :

TTCCTGGGGC TCCGGGGCGC GGAGAAAGCTG CATCCCAGAG GAGCGCGTCC AGGAGCGGAC 60

CCGGGAGTGT TTCAAGAGCC AGTGACAAGG ACCAGGGGCC CAAGTCCCAC CAGCCATGCA	120
GACCTGCCCC CTGGCATTCC CTGGCCACGT TTCCCAGGCC CTTGGGACCC TCCTGTTTT	180
GGCTGCCTCC TTGAGTGCTC AGAATGAAGG CTGGGACAGC CCCATCTGCA CAGAGGGGT	240
AGTCTCTGTG TCTTGGGCG AGAACACCGT CATGTCTGC AACATCTCCA ACGCCTTCTC	300
CCATGTCAAC ATCAAGCTGC GTGCCACGG GCAGGAGAGC GCCATCTCA ATGAGGTGGC	360
TCCAGGCTAC TTCTCCCAGG ACGGCTGGCA GCTCCAGGTT CAGGGAGGCG TGGCACAGCT	420
GGTGATCAA GGCGCCCGGG ACTCCCAGTC TGGGCTGTAC ATGTGGCACC TCGTGGGACA	480
CCAGAGAAAT AACAGACAAG TCACGCTGGA GGTTTCAGGT GCAGAACCCC AGTCCGCC	540
CGACACTGGG TTCTGGCCTG TGCCAGCGGT GGTCACTGCT GTCTTCATCC TCTTGGTCGC	600
TCTGGTCATG TTCGCCTGGT ACAGGTGCCG CTGTTCCCAG CAACGCCGGG AGAAGAAGTT	660
CTTCCTCCTA GAACCCAGA TGAAGGTGCG AGCCCTCAGA GCAGGAGCCC AGCAGGGCCT	720
GAGCAGAGCC TCCGCTGAAC TGTGGACCCC AGACTCCGAG CCCACCCCAA GGCGCTGGC	780
ACTGGTGTTC AAACCCCTCAC CACTTGGAGC CCTGGAGCTG CTGTCCCCCC AACCTTGTT	840
TCCATATGCC GCAGACCCAT AGCCGCCTGC AAGGAAGAGA GGACACAGGA GTAGCCACCC	900
TGAGTGCCGA CCTTTGGTGG CGGGGGCCTG GGTCTCTCGT CCCCACCCGG AAGGGCACAA	960
GACACCGGGC TTTGCTTGGC AAGGCTTGGG GCCTCTGTG GTCAACCCAG TTCCCTTGGG	1020
TGCCGTTGCA GAACCCCTTA GCCCCTTCCA ACGTCGACCA GGTT	1064

(2) INFORMATION FOR SEQ ID NO: 110:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1031 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110 :

AGTTCTTGCA GGTGCCGGCG GTGACGCGGG CTTACACCGC AGCCTGTGTC CTCATCCACC	60
GCCGCGGTGC AGCTGGAGCT CCTCAGCCCC TTTCAACTCT ACTTCAACCC GCACCTTGTG	120
TTCCGGAAGT TCCAGGTGAG GCCGCCTCGC GCCGCGCACC TGGGGCCCGA CCCACCCACC	180
CCGCACCTGA CCGCCCGTCC CCCGTAGGTC TGGAGGCTCG TCACCAACTT CCTCTTCTTC	240
GGGCCCCCTGG GATTCAAGCTT CTTCTTCAAC ATGCTCTTCG TGTATCCTGC GCCTGCGGAC	300
ACGGGCTGGG TGGAGGGCAG GCCGGCCGGG CTGGGAGAGA GGCGGGGACG GGGAAACTGA	360

PF-0459 US

GGCCCCGCCT	GGTGGCACTT	CCTATAACCGA	CGCCGTAGGT	TCCGCTACTG	CCGCATGCTG	420
GAAGAGGGCT	CCTTCCGCGG	CCGCACGGCC	GACTTCGTCT	TCATGTTCT	CTTCGGGGC	480
GTCCTTATGA	CCGTATCCTT	CCCGCAGGCT	CTGGAACCTC	GGGCTAGGGC	GCCTCGGCGT	540
CCAGCCTGTG	TTGGTCCTGG	GGCCAACACA	GCCATGCCAG	AGAGGGACAC	AGTCGCTGTC	600
TCCAGCTTAG	CACCGTTCCCT	GCCTTGGCG	CTCATGGGCT	TCTCGCTGCT	GCTGGGCAAC	660
TCCATCCTCG	TGGACCTGCT	GGGGATTGCG	GTGGGCCATA	TCTACTACTT	CCTGGAGGAC	720
GTCTTCCCCA	ACCAGCCTGG	AGGCAAGAGG	CTCCTGCAGA	CCCCTGGCTT	CCTAAAGCTG	780
CTCCTGGATG	CCCCTGCAGA	AGACCCCAAT	TACCTGCC	TCCCTGAGGA	ACAGCCAGGA	840
CCCCATCTGC	CACCCCCGCA	GCAGTGACCC	CCACCCAGGG	CCAGGCCTAA	GAGGCTTCTG	900
GCAGCTTCCA	TCCTACCCAT	GACCCCTACT	TGGGGCAGAA	AAAACCCATC	CTAAAGGCTG	960
GGCCCATGCA	AGGGCCCACC	TGAATAAAC	GAATGAGCTG	CAAAAAAAA	AAAAAAGGGC	1020
GGCCGTGCG	A					1031

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSTUT12
- (B) CLONE: 1812375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111 :

GCTGGATAAG	ACACCAGGGG	AGTCACTACA	TGGTTACCGC	ATCTGTATCC	AGGCCATCCT	60
GCAAGACAAG	CCCAAGATTG	CCACGGCAAA	CCTAGGCAAG	TTCCTGGAAC	TGCTGAGGTC	120
CCACCAGAGC	CGACCAGCAA	AGTGTCTCAC	CATCATGTGG	GCCCTGGTC	AAGCAGGTTT	180
TGCCAACCTC	ACCGAGGGAC	TGAAAGTGTG	GCTGGGGATC	ATGCTGCCTG	TGCTGGGCAT	240
CAAGTCTCTG	TCTCCCTTG	CCATCACATA	CCTGGATCGG	CTGCTCCTGA	TGCATCCCAA	300
CCTTACCAAG	GGCTTCGGCA	TGATTGGCCC	CAAGGACTTC	TTCCCACCTC	TGGACTTTGC	360
CTATATGCCG	AACAACCTCC	TGACACCCAG	CCTGCAGGAG	CAGCTGTGTC	AGCTCTACCC	420
CCGACTGAAA	ATGCTGGCAT	TTGGAGCAA	GCCGGATTCC	ACCCTGCATA	CCTACTTCCC	480
TTCTTCTG	TCCAGAGCCA	CCCCTAGCTG	TCCCCCTGAG	ATGAAGAAAG	AGCTCCTGAG	540
CAGCCTGACT	GAGTGCCTGA	CGGTGGACCC	CCTCAGTGCC	AGCGTCTGGA	GGCAGCTGTA	600

CCCTAACGAC CTGTCACAGT CCAGCCTCT GCTGGAGCAC TTGCTCAGCT CCTGGGAGCA 660
GATTCCAAG AAGGTACAGA AGTCTTGCA AGAAACCATT CAGTCCTCA AGCTTACCAA 720
CCAGGAGCTG CTGAGGAAGG GTAGCAGTAA CAACCAGGAT GTCGTACCT GTGACATGGC 780
CTGCAAGGGC CTGTTGCAGC AGGTCAGGG TCCTCGGCTG CCCTGGACGC GGCTCCTCCT 840
GTTGCTGCTG GTCTCGCTG TAGGCTTCCT GTGCCATGAC CTCCGGTCAC ACAGCTCCTT 900
CCAGGCCTCC CTTACTGGCC GGTTGCTTCG ATCATCTGGC TTCTTACCTG CTAGCCAACA 960
AGCGTGTGCC AAGCTCTACT CCTACAGTCT GCAAGGCTAC AGCTGGCTGG GGGAGACACT 1020
GCCGCTCTGG GGCTCCCACC TGCTCACCGT GGTGCGGCCAG AGCTGCAGC TGGCCTGGC 1080
TCACACCAAT GCCACAGTCA GCTTCCTTTC TGCCCACGTGC TGCTGCTGCC 1140
TGGTGACAGT CTCACCCAGTC TCTCTCAGAG GCTACAGATC CAGCTCCCCG ATTCCGTGAA 1200
TCAGCTACTC CGCTATCTGA GAGAGCTGCC CCTGCTTTTC CACCAGAATG TGCTGCTGCC 1260
ACTGTGGCAC CTCTTGCTTG AGGCCCTGGC CTGGGCCAG GAGCACTGCC ATGAGGCATG 1320
CAGAGGTGAG GTGACCTGGG ACTGCATGAA GACACAGCTC AGTGAGGCTG TCCACTGGAC 1380
CTGGCTTGC CTACAGGACA TTACAGTGGC TTTCTGGAC TGGGCACTTG CCCTGATATC 1440
CCAGCAGTAG GCCCTGCCTT CCTGGCCACT GATTCTGCA TGGGTAGACC ATCCAAGACT 1500
GCAGCGGGTA GAAGGTGGCA GTTCTTCATG GGAGTCTTT TAACTGGTG CCTGAGTTCT 1560
CTCCTAGGCA AGTGGCCAGT TGCCTCCACC TCAGTTCTTC CATCTTGGT GGGGACAGGG 1620
CCCAGCAGCA TCTCAGCCTC CTACCCACAA TTCCACTGAA CACTTTCTG GCCCTACTGC 1680
ACATGGCCCC CAGCCTCCAT CCTTGTGCTG GTAGCCTCTC ACAACTCCGC CCTTGCCCTC 1740
TGCCTTCCAC TTCCCTCCAT CTCATTTCTA AACCCCAAAAC AGCTCATCTC TAAAAAAGATA 1800
GAACTCCCAG CAGGTGGCTT CTGTGTTCTT CTGACAAATG ATTCCCTGCTT CTCCAGACTT 1860
TAGCAGCCTC CTGTTCCCAT TCTTGGTCAC AGCTCTAGCC ACAGCAGAAG GAAAGGGGCT 1920
TCCAGAAGAA TATAGCACCG CATTGGGAAA CAGCAGCCTC ACCTCCACCT GAAGCCTGGG 1980
TGTGGCTGTC AGTGGACATG GGGAGCTGGA TGGAAATGCC TCTCACTTCA AAATGCCAG 2040
CCTGCCCAA ATGCCTCTAA GCCCCTCCCT GTCCCCCTCCC TTGTAGTCCT ACTTCTTCCA 2100
ACTTTCCATT CCCCACATG CTGGGGGTCT TGGTCACAAG GCTCAGCTTC TCTCCACTGT 2160
CCATCCCTCC TATCATCTGT AGAGCAGAGC ACAGGCAGTT GTGTGCCTTG GGCCCAGGG 2220
ACCCTCCATC AACCTGAGAC AGGACTCAGT ATATGGTTCT TGGGTATGCC CTACCAGGTG 2280
GAATAAAGGA CACAGATTTG AAAAAAAAAA AAAAAA 2316

(2) INFORMATION FOR SEQ ID NO: 112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1169 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: PROSN0T20
 - (B) CLONE: 1818761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112 :

AGCAAGGAGC CAGAGGCCAT GCAGTGGCTC AGGGTCCGTG AGTCGCCTGG GGAGGCCACA 60
 GGACACAGGG TCACCATGGG GACAGCCGCC CTGGGTCCCG TCTGGCAGC GCTCCTGCTC 120
 TTTCTCCTGA TGTGTGAGAT CCCTATGGTG GAGCTCACCT TTGACAGAGC TGTGCCAGC 180
 GGCTGCCAAC GGTGCTGTGA CTCTGAGGAC CCCCTGGATC CTGCCCATGT ATCCTCAGCC 240
 TCTTCCTCCG GCCGCCCA CGCCCTGCCT GAGATCAGAC CCTACATTAA TATCACCATC 300
 CTGAAGGGTG ACAAAAGGGGA CCCAGGCCA ATGGGCCTGC CAGGGTACAT GGGCAGGGAG 360
 GGTCCCCAAG GGGAGCCTGG CCCTCAGGGC AGCAAGGGTG ACAAGGGGA GATGGGCAGC 420
 CCCGGCGCCC CGTGCCAGAA GCGCTTCTTC GCCTTCTCAG TGGGCCGCAA GACGGCCCTG 480
 CACAGCGGCG AGGACTTCCA GACGCTGCTC TTCGAAAGGG TCTTGTGAA CCTTGATGGG 540
 TGCTTGACA TGGCGACCGG CCAGTTGCT GCTCCCTGC GTGGCATCTA CTTCTTCAGC 600
 CTCAATGTGC ACAGCTGGAA TTACAAGGAG ACGTACGTGC ACATTATGCA TAACCAGAAA 660
 GAGGCTGTCA TCCTGTACGC GCAGCCCAGC GAGCGCAGCA TCATGCAGAG CCAGAGTGTG 720
 ATGCTGGACC TGGCCTACGG GGACCGCGTC TGGGTGCGGC TCTTCAAGCG CCAGCGCGAG 780
 AACGCCATCT ACAGCAACGA CTTCGACACC TACATCACCT TCAGCGGCCA CCTCATCAAG 840
 GCCGAGGACG ACTGAGGGCC TCTGGGCCAC CCTCCCGGCT GGAGAGCTCA GGTGCTGGTC 900
 CCGTCCCCTG CAGGGCTCAG TTTGCACTGC TGTGAAGCAG GAAGGCCAGG GAGGTCCCCG 960
 GGGACCTGGC ATTCTGGGGA GACCCTGCTT CTATCTTGGC TGCCATCATC CCTCCCAGCC 1020
 TATTCTGCT CCTCTCTTCT CTCTTGGACC TATTTAAGA AGCTTGCTAA CCTAAATATT 1080
 CTAGAACTTT CCCAGCCTCG TAGCCCAGCA CTTCTCAAAC TTGGAAATGC ATGCGAATCA 1140
 CCCGGGGTTC GTGTTAAATG CAGATTCTG

1169

(2) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1530 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: GBLATUT01
(B) CLONE: 1824469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113 :

TCACAGACTG CGGAGTGGGT CAGGGGCTGC GAGGGCTGCC CCAAGTCCTA CCGGGTTTGC 60
ACGGGCGCGC CCGGCTCCGC CCGCAAGTGC GCCTTCCTGA CTTACTGCTG GGTGCGCGGG 120
GCTGGGGGTG CGAGTACAC CCCTGAAGTC TCTTCCTGGG CGACCTCCGG GGCCTCATTC 180
TAGGCCTCCT TAAAGAGAAG GATCTAAATT AGGAAAAGGA AGTGCCTTA TCCACGACCA 240
AGCTCTTCCA CCTGCGGAGC TCGCTTAGTC TGACACCTCAA CCGTGCAGGAA AGTGAUTGCC 300
CTGTTTACTG AGGAAAAACT GGGGCTCAGA AAGATACCAT GAGTAGTTG AAACAGGAAC 360
AAAATCTTCT GAAAGCTCGG AGCAGAAGCC TTTTGTTCA ACATGGAGGA AAAAAGACGG 420
CGAGCCCGAG TTCAGGGAGC CTGGGCTGCC CCTGTTAAAA GCCAGGCCAT TGCTCAGCCA 480
GCTACCACTG CTAAGAGCCA TCTCCACCAG AAGCCTGGCC AGACCTGGAA GAACAAAGAG 540
CATCATCTCT CTGACAGAGA GTTTGTGTT AAAGAACCTC AGCAGGTTAGT ACGTAGAGCT 600
CCTGAGCCAC GAGTGATTGA CAGAGAGGGT GTGTATGAAA TCAGCCTGTC ACCCACAGGT 660
GTATCTAGGG TCTGTTTGTG TA TCCTGGCTTT GTTGACGTGA AAGAAGCTGA CTGGATATTG 720
GAACAGCTTT GTCAAGATGT TCCCTGGAAA CAGAGGACCG GCATCAGAGA GGATATAACT 780
TATCAACAAAC CAAGACTTAC AGCATGGTAT GGAGAACTTC CTTACACTTA TTCAAGAAC 840
ACTATGGAAC CAAATCCTCA CTGGCACCCCT GTGCTGCGCA CACTAAAGAA CCGCATTGAA 900
GAGAACACTG GCCCACACCTT CAACTCCTTA CTCTGCAATC TTTATCGCAA TGAGAAGGAC 960
AGCGTGGACT GGCACAGTGA TGATGAACCC TCACTAGGGA GGTGCCCAT TATTGCTTCA 1020
CTAAGTTTG GTGCCACACG CACATTGAG ATGAGAAAGA AGCCACCAAG AGAAGAGAAT 1080
GGAGACTACA CATATGTGGA AAGAGTGAAG ATACCCCTGG ATCATGGTAC CTTGTTAAC 1140
ATGGAAGGAG CGACACAAGC TGACTGGCAG CATCGAGTGC CCAAAGAATA CCACTCTAGA 1200
GAACCGAGAG TGAACCTGAC CTTTCGGACA GTCTATCCAG ACCCTCGAGG GGCACCCCTGG 1260
TGACGTCAGA GCTTGAGAG AGAAGCTTCA CTGAAACGGG GCAAACCTTC CACTGAGAAG 1320
CCACTTCAAG AGGCTGGTGC TGCTAGATCT CATGATGTGG CTGTTGGGAA GATGGTGGGG 1380
TTTGTGTTGCC AGCTTGGAGT CCTATTAAAT GAAAGCCAGC AACTCATGTT GGTAATAGGT 1440
CTACTGTGGG AACAGTTATC CCTAACCAACA GCTCAAAATC GCTATCATCT TTAGGCAAAT 1500

TAAAATCTAT GTGGCAGTGA AAAAAAAAAA

1530

(2) INFORMATION FOR SEQ ID NO: 114:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: PROSNOT19
 - (B) CLONE: 1864292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114 :

AGCTCGTACC CCTCGAGTGA AATTCTGAAA TGAAGATGGA GGAGGCAGTG GGAAAAGTTG 60
AAGAAACTCAT TGAGTCCGAA GCCCCACCAA AAGCATCTGA ACAAGAGACA GCCAAGGAGG 120
AAGATGGATC TGTAGAACTG GAATCTCAAG TTCAGAAAGA TGGTGTAGCG GATTCTACAG 180
TTATTTCTTC AATGCCCTGC TTGTTGATGG AACTGAGAAG GGACTCTTCT GAGTCTCAGT 240
TAGCATCCAC AGAGAGTGAC AAGCCTACAA CTGGCCGAGT TTATGAGAGT GACCCCTCTA 300
ATCACTGCAT GCTTCCCCT TCCTCTAGTG GTCACCTGGC TGATTCAGAT ACGTTGTCTT 360
CCGCAGAAGA GAATGAACCC TCTCAGGCAG AAACGGCGGT AGAAGGAGAC CCTTCAGGAG 420
TGTCTGGTGC CACAGTTGGG CGCAAGTCTA GGCGGTCCCG ATCTGAAAGT GAAACTTCCA 480
CTATGGCTGC CAAGAAAAAC CGGCAATCCA GTGATAAACCA GAATGGCCGA GTCGCCAAGG 540
TTAAAGGTCA TCGGAGCCAA AAGCACAAGG AGAGGATCAG GCTACTGAGG CAGAACGGG 600
AGGCTGCTGC AAGGAAGAAA TATAACCTGC TGCAGGACAG TAGTACCAAGT GATAGTGACC 660
TGACTTGTGA CTCAAGCACG AGCTCATCAG ATGATGATGA AGAGGTTCA GGGAGCAGCA 720
AGACAATCAC TGCAGAGATA CCAGATGGAC CTCCAGTTGT AGCTCATTAT GATATGTCTG 780
ACACCAACTC TGACCCAGAA GTGGTAAATG TGGACAATT ATTGGCGGCT GCAGTAGTTC 840
AAGAGCACAG TAATTCTGTA GGCGGCCAGG ACACAGGAGC TACCTGGAGG ACCAGCGGGC 900
TTCTAGAGGA GCTGAATGCA GAGGCAGGTC ATTGGATCC AGGATTCTA GCAAGTGACA 960
AAACATCTGC TGGCAATGCG CCACTCAATG AAGAAATTAA CATTGCGTCT TCAGATAGTG 1020
AAGTAGAGAT TGTGGGAGTT CAGGAACATG CAAGGTGTGT TCATCCTCGA GGTGGTGTGA 1080
TTCAGAGTGT TTCTTCATGG AAGCATGGCT CGGGCACGCA GTATGTTAGC ACCAGGCAA 1140
CACAGTCATG GACTGCTGTG ACTCCCCAGC AGACTTGGGC TTCACCAGCA GAAGTTGTG 1200
ACCTTACCTT GGATGAGGAT AGCAGGCGTA AATACCTACT GTAATACAAT GTCACTGTGT 1260

TTCCTCTGCA CTGTTCCCTT CCACCTCCTC ATCCTCTTG TGACATGGAA GTTCATTGTC 1320
 ATAGGGGTAC GGAGCT 1336

(2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1742 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: THP1NOT01
 - (B) CLONE: 1866437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115 :

CCCCCGCCCC CTCCCCGCC GCCTTCCCGG TGACCTTCAG GGGCCCGGGT GGCGGGCGCA 60
 GGCCCCCTGCG GCGGCCGGCGG GATGTTCGTG CAGGAGGAGA AGATCTTCGC GGGCAAGGTG 120
 CTGCGGCTGC ACATCTGCGC GTCCGACGGC GCCGAGTGGC TGGAGGAGGC CACCGAGGAC 180
 ACCTCGGTGG AGAACGCTCAA GGAGCGCTGC CTCAAGCACT GTGCTCATGG GAGCTTAGAA 240
 GATCCCCAAA GTATAACCCA TCATAAAATTA ATCCACGCTG CCTCAGAGAG GGTGCTGAGT 300
 GATGCCAGGA CCATCCTGGA AGAGAACATC CAGGACCAAG ATGTCCTATT ATTGAAAAAA 360
 AAGCGTGCTC CATCACCACT TCCCAAGATG GCTGATGTCT CAGCAGAAGA AAAGAAAAAA 420
 CAAGACCAGA AAGCTCCAGA TAAAGAGGCC ATACTGCGGG CCACCGCCAA CCTGCCCTCC 480
 TACAACATGG ACCGGGCCGC GGTCCAGACC AACATGAGAG ACTTCCAGAC AGAACTCCGG 540
 AAGATACTGG TGTCTCTCAT CGAGGTGGCG CAGAAGCTGT TAGCGCTGAA CCCAGATGCG 600
 GTGGAATTGT TTAAGAACGGC GAATGCAATG CTGGACGAGG ACGAGGATGA GCGTGTGGAC 660
 GAGGCTGCC TGCGGCAGCT CACGGAGATG GGCTTCCGG AGAACAGAGC CACCAAGGCC 720
 CTTCAGCTGA ACCACATGTC GGTGCCTCAG GCCATGGAGT GGCTAATTGA ACACGCAGAA 780
 GACCCGACCA TAGACACGCC TCTTCCTGGC CAAGCTCCCC CAGAGGCCGA GGGGCCACA 840
 GCAGCTGCCT CCGAGGCTGC CGCGGGAGCC AGCGCCACCG ATGAGGAGGC CAGAGATGAG 900
 CTGACGGAAA TCTTCAAGAA GATCCGGAGG AAAAGGGAGT TTCGGGCTGA TGCTCGGGCC 960
 GTCATTTCCC TGATGGAGAT GGGGTTCGAC GAGAAAGAGG TGATAGATGC CCTCAGAGTG 1020
 AACAAACAACC AGCAGAACATGCC CGCGTGCAG TGGCTGCTGG GGGACCGGAA GCCCTCTCCG 1080
 GAGGAGCTGG ACAAGGGCAT CGACCCCGAC AGTCCTCTCT TTCAGGCCAT CCTGGATAAC 1140
 CCGGTGGTGC AGCTGGGCCT GACCAACCCG AAAACATTGC TAGCATTGAA AGACATGCTG 1200

PF-0459 US

GAGAACCCAC TGAACAGCAC CCAGTGGATG AATGATCCAG AAACGGGCC TGTATGCTG 1260
CAGATCTCTA GAATCTTCCA GACACTAAAT CGCACGTAGG TGGCGTTGTT CCACTCGGCT 1320
ATCAGGCCAC AGCAGCCCC CGAGACCGGG CAGAGTGGAC CTCACCTGGA 1380
AACTCACCTT CAGCGCCTCA GCCCTGGACT GTTAGAGGTG CTGCAGCTGC TCCTGCTCTC 1440
TGATCTTATT GCTTATAAAC TTTGGTGACG GTAGTGTGTA AGGCCGTATT TTTAGCATCT 1500
GACAGGTGTT TACAAAAAAG TGGTTGTCGC ACTGGGAAGT GGAGTGATGG CCTCGTCTCC 1560
AGTGCTCCTC TGGGCTCTG AGTTGCTGCT TGAATTGCCG TGTAGACATT TGCTGGAGA 1620
GTCCACTTGT TATTTGACGG AGGTAGGTT CAACCCAGAG TTAATGTCAA GCATGCTAAT 1680
TTAACTAGTC ACTCACAGAT GACTTTCTT TAATAAGTC CCTTTCTA TTAAAAAAA 1740
AA 1742

(2) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1074 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: SKINBIT01
(B) CLONE: 1871375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116 :

GCGGTGCAGA GGAAGCACAA CCTCTACCGG GACAGCATGG TCATGCACAA CAGCGACCC 60
AACCTGCACC TGCTGGCCGA GGGCGCCCCC ATCGACTGGG GCGAGGAGTA CAGCAACAGC 120
GGCGGGGGCG GCAGCCCAGC CCCAGCACCC CGGAGTCAGC CACCCCTCTCG GAAAAGCGAC 180
GGCGCGCCAA GCAGGGTGGTC TCTGTGGTCC AGGATGAGGA GGTGGGGCTG CCCTTGAGG 240
CTAGCCCTGA GTCACCACCA CCTGCGTCCC CGGACGGTGT CACTGAGATC CGAGGCCTGC 300
TGGCCCAAGG TCTGCGGCCT GAGAGCCCCC CACCAGCCGG CCCCCTGCTC AACGGGGCCC 360
CCGCTGGGGA GAGTCCCCAG CCTAAGGCCG CCCCCGAGGC CTCCTCGCCG CCTGCCTCAC 420
CCCTCCAGCA TCTCCTGCCT GGAAAGGCTG TGGACCTTGG GCCCCCCAAG CCCAGCGACC 480
AGGAGACTGG AGAGCAGGTG TCCAGCCCCA GCAGCCACCC CGCCCTCCAC ACCACCACCG 540
AGGACNANTT TCAAGGGGTG CAAGAATTGA AGNTTCNTAA GGGCCAANTT GGGGGTCCCC 600
TTGACTTGGN TTGGNAANAT TGGGGCAAAA AGGGCCGGTT TTCCCCNTTT CCCGGGANAC 660
CCCAAGGGAA AGGGGNTTCA AAGCTTCTN GGGGGGGAAA GGGGGAANCC CTTGGGTNTT 720

TTGTTGCCN TTTGTGANCA NCAGCGAGGA GAGTGCAAAG GTGCAGAGTN AGTTNTAGGN 780
 CANTGGGTCC CTGACTGCTG CANATGGTAA GGNCGTTNNC TTGTGGACCC AAGGCAGGNA 840
 AAGNTGTGGG GAGGGAAAGCT GGTNTGTGCN TTGTGGGTGG AAGCAGGGAN GGCTGTGTG 900
 NANGGCAGGG AGAGGGCNAA NTGAGTTATT TATTGGGGTT CANGTGAAAA GTTTCTTGNN 960
 CCCTGTNTTG TGTTNCTGTG GGATTGATTN TAAGATNGNN AGGGTNGGT TTTTGGGGTT 1020
 TTCCTGGTTG GTGGCCAAAN GGGTTGGAAA ATNGNTGGGG GGGGNTTGGGA NAAT 1074

(2) INFORMATION FOR SEQ ID NO: 117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1454 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: LEUKNOT03
 - (B) CLONE: 1880830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117 :

CCCGGGGGAG GCCTGACCCC CTCCGCACCA CCGTACGGAG CCGCATTCC CCCGTTCCC 60.
 GAGGGGCATC CAGCCGTGTT GCCTGGGGAG GACCCACCCC CCTATTCACT CTTAACTAGC 120
 CCGGACAGTG GGAGTGCCCC TATGATCACC TGCCGAGTCT GCCAATCTCT CATCAACGTG 180
 GAAGGCAAGA TGCATCAGCA TGTAGTCATA TGTGGTGTCT GCAATGAAGC CACCCCAATC 240
 AAGAATGCAC CCCCAGGGAA AAAATATGTT CGATGCCCT GTAACTGTCT CCTTATCTGC 300
 AAAGTGACAT CCCAACGGAT TGCATGCCCT CGGCCCTACT GCAAAAGAAT CATCAACCTG 360
 GGGCCTGTGC ATCCCGGACC TCTGAGTCCA GAAACCCAAAC CCATGGGTGT CAGGGTTATC 420
 TGTGGACATT GCAAGAATAC TTTTCTGTGG ACAGAGTTCA CAGACCGCAC TTTGGCACGT 480
 TGTCTCACT GCAGGAAAGT GTCATCTATT GGGCGCAGAT ACCCACGTAA GAGATGTATC 540
 TGCTGCTTCT TGCTTGGCTT GCTTTGGCA GTCACTGCCA CTGGCCTTGC CTTTGGCAC 600
 TGGAAAGCATG CACGGCGATA TGGAGGCATC TATGCAGCCT GGGCATTGT CATCCTGTG 660
 GCTGTGCTGT GTTGGGGCCG GGCTCTTAT TGGGCCTGTA TGAAGGTCAG CCACCCCTGTC 720
 CAGAACTTCT CCTGAGCCTG ATGACCCACA GACTGTGCCT GGCCCCCTCCC TGGTGGGGAC 780
 AGTGACACTA CGAAGGGAGC TGGGGTAGTT AAAGGCTCCC GGGGCTTCTA GAAGGAAGCC 840
 AAGCAGCTGC CTTCTTTTC CCTGGGGAGA GGTAGGAAGG AACCAAGGCC TCACCTAGGT 900
 TTGGAGGGGC AGATAAGAGC ACTGCTGACC ATCTGCTTTC CTCCAAGGGT TGCTGTGTCT 960

AGGGTGAAGT AGGCAAAACG TTGCCCTAA AACTGGGCC TGAAGACGGT TCCAGCCTG 1020
 TCCTTCCTGT GTGCTCCCTG AGAGCCATTC CTGTCCCTA CACATTCCAG GGCAGGGTGG 1080
 GGGTGGGTAG CCCTGGGGGT TCCCCCTCCCT CTTGTGCACC ATTAGGACTT TGCTGCTGCT 1140
 ATTGCACCTTC ACCAGAGGTT GGCTCTGGCC TCAGTACCCCT CAGTCTCCTC TCCCCACATT 1200
 GTGTCCCTGTG GGGGTGGGGT CAGCCGCTGC TCTGTACAGA ACCACAGGAA CTGATGTGTA 1260
 TATAACTATT TAATGTGGGA TATGTTCCCC TATTCCCTGTA TTTCCCTAA TTCCTCCTCC 1320
 CGACCTTTT TACCCCCCA GTTGCAGTAT TTAACTGGGC TGGGTAGGGT TGCTCAGTCT 1380
 TTGGGGGAGG TTAGGGACTT ATCCTGTGCT TGTAAATAAA TAAGGTCATG ACTCTAAAAA 1440
 AAAAAAAAGG GCGG 1454

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2071 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: OVARNOT07
 (B) CLONE: 1905325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118 :

AGCTTTGAAT TCCTGTATCT GAGAACGGAT CGTTCGAGGT GGTGGAGGGG GTTGGAATTG 60
 GGGACCTACG GAAGGCTCAG CTCTGCCAG GCCAAATTGA GACATGTCTG ACACAAGCGA 120
 GAGTGGTGCA GGTCTAACTC GCTTCCAGGC TGAAGCTTCA GAAAAGGACA GTAGCTCGAT 180
 GATGCAGACT CTGTTGACAG TGACCCAGAA TGTGGAGGTC CCAGAGACAC CGAAGGCCCTC 240
 AAAGGCAGTG GAGGTCTCAG AGGATGTGAA GGTCTAAAAA GCCTCTGGGG TCTCAAAGGC 300
 CACAGAGGTC TCAAAGACCC CAGAGGCTCG GGAGGCACCT GCCACCCAGG CCTCGTCTAC 360
 TACTCAGCTG ACTGATAACCC AGGTTCTGGC AGCTGAAAAC AAGAGTCTAG CAGCTGACAC 420
 CAAGAAACAG AATGCTGACC CGCAGGCTGT GACAATGCCT GCCACTGAGA CCAAAAAGGT 480
 CAGCCATGTG GCTGATAACAA AGGTCAATAC AAAGGCTCAG GAGACTGAGG CTGCACCCCTC 540
 TCAGGCCCA GCAGATGAAC CTGAGCCTGA GAGTGCAGCT GCCCAGTCTC AGGAGAATCA 600
 GGATACTCGG CCCAAGGTCA AAGCCAAGAA AGCCCGAAAG GTGAAGCATH TGGATGGGA 660
 AGAGGATGGC AGCAGTGATC AGAGTCAGGC TTCTGGAACC ACAGGTGGCC GAAGGGTCTC 720
 AAAGGCTCTA ATGGCCTCAA TGGCCCGCAG GTTTCAAGGG GTCCCATAGC CTTTGGGCC 780

PF-0459 US

CGCAGGATTCAAGGACTCGG TTGGCTGCTT GGGCCCGGAG AGCCTGCTC TCCCTGAGAT 840
CACCTAAAGC CCGTAGGGCA AGGCTCGCCG TAGAGCTGCC AAGCTCCAGT CATCCCAAGA 900
GCCTGAAGCA CCACCACCTC GGGATGTGGC CCTTTGCAA GGGAGGGCAA ATGATTTGGT 960
GAAGTACCTT TTGGCTAAAG ACCAGACGAA GATTCCCATC AAGCGCTCGG ACATGCTGAA 1020
GGACATCATC AAAGAATACA CTGATGTGTA CCCCGAAATC ATTGAACGAG CAGGCTATT 1080
CTTGGAGAAG GTATTGGGA TTCAATTGAA GGAAATTGAT AAGAATGACC ACTTGTACAT 1140
TCTTCTCAGC ACCTTAGAGC CCACTGATGC AGGCATACTG GGAACGACTA AGGACTCACC 1200
CAAGCTGGGT CTGCTCATGG TGCTTCTTAG CATCATCTTC ATGAATGGAA ATCGGTCCAG 1260
TGAGGCTGTC ATCTGGGAGG TGCTGCGCAA GTTGGGGCTG CGCCCTGGGA TACATCATTC 1320
ACTCTTGAG GACGTGAAGA AGCTCATCAC TGATGAGTTT GTGAAGCAGA AGTACCTGGA 1380
CTATGCCAGA GTCCCCAATA GCAATCCCC TGAATATGAG TTCTTCTGGG GCCTGCGCTC 1440
TTACTATGAG ACCAGCAAGA TGAAAGTCCT CAAGTTGCC TGCAAGGTAC AAAAGAAGGA 1500
TCCCAAGGAA TGGGCAGCTC AGTACCGAGA GGCATGGAA GCAGATTGA AGGCTGCAGC 1560
TGAGGCTGCA GCTGAAGCCA AGGCTAGGGC CGAGATTAGA GCTCGAATGG GCATTGGGCT 1620
CGGCTCGGAG AATGCTGCCG GGCCCTGCAA CTGGGACGAA GCTGATATCG GACCCTGGGC 1680
CAAAGCCCCG ATCCAGGCAG GAGCAGAAGC TAAAGCCAAA GCCCAAGAGA GTGGCAGTGC 1740
CAGCACTGGT GCCAGTACCA GTACCAATAA CAGTGCCAGT GCCAGTGCCA GCACCAGTGG 1800
TGGCTTCAGT GCTGGTGCCTA GCCTGACCGC CACTCTCAC 1860
TTTGGGCTCT TCGCTGGCCT 1860
TGGTGGAGCT GGTGCCAGCA CCAGTGGCAG CTCTGGTGCC TGTGGTTCT CCTACAAGTG 1920
AGATTTAGA TATTGTTAAT CCTGCCAGTC TTTCTCTTCA AGCCAGGGTG CATCCTCAGA 1980
AACCTACTCA ACACAGCACT CTAGGCAGCC ACTATCAATC AATTGAAGTT GACACTCTGC 2040
ATTAATCTA TTTGCCATTT CAAAAAAA A 2071

(2) INFORMATION FOR SEQ ID NO: 119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1236 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: BRSTTUT01
 - (B) CLONE: 1919931
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119 :

PF-0459 US

ACCTGGGACC CCCAGAACGG CCGCCCCTTT TTTTTTTTT TTTTTTTTTT TTTTTTTTTT 60
TTTTTTTTT TTTTTTTTT TTTTTTTTT TTTTTTTTAG AAGGTTGAAA CCAGGCTTAT 120
TTATTTCAT CTTCTTCTG CCATCTTTA ACCAACCTTC TCAGAATAAA ATGTGATTT 180
TGAGACAGAA TGAAACACAT ATCCAAATTT TAATACAGTA AGAATAGGTA TCCTGAATAA 240
ATGAGAACTC TAGAAAATCA AGGTTCAAA ATTCTACCTC TCCTGGGAGT TAAAGAAGTT 300
TGGCAGAAAC AGAACAAATT AATCAGCAGA TTCATCACCT GCCAATTTC TCTGTACAAT 360
TTTCTTGATT CTGGGAGCAT CTGGGTCCAG GCAGATTTTC CTCCCATCCT TCAGTGTGGC 420
TGCTTCTGT TTCATCCATG GACCCTGCAA GAAATTGCC CATGTTCTG TTTGTGCATC 480
ACTGAGAAAG GAAGCATGAA GGTCGCACAG GTCAGGCCAT TCCATTGCC TCCTGGTGCC 540
GGGTTTGCCC TCCCAATCCT GGGGTTGCTT CAGGGGCTTG TCATTCTCCA TAGTCCCCTC 600
CACATTCTC AGGTTCTGC TCAAAAGTCA CCTTTGGAG GGGTCTCCAC CTGTCACTGT 660
GTTTGTAAAGA GCTCCTTCAG TTTCTTCTA GCTCATCTCA CTCTGGTAAT GTCTTGATT 720
ACCACCACCA TCTGACCTGG TCTTATGACC TGTTAGCTT CTTCATCAGA CGTGAGCACC 780
AGGATGGCAG GGGCCTCATC TGTCCCTGTC CTCCGTGGC CTGGGTCCATA GCACCATGTC 840
TGGTACAGTG TAGATGCTCA AGGGAAGTTT ACTTTGTAAA ACCACTTACC TGGGAGATGT 900
TACTGTTAGT CTAACCTGTA CCATTTGTA AACCTCCAGC CATTTCAG ACTCTGATCA 960
CAGTGAAACG TTCCATGGGA ACTTGGGCCA TGAGAAACAT CCTTCCTAAC CACGTGACTG 1020
CAGAAACATC CTTATCGCGT CCTCCTGGC AAAGGCCAA CAGCCTGACT GCAGGGACAT 1080
CCTTGCCATA TCCTGCTGGG CAGCAAGCTC TACCACCCAG ATCCCTCCCT CCCAGTCCCA 1140
TGATTACCCC AGCCTGTGAG TGGCAGTTGG TGCTGGCACT AAGCTGGTTT CCTCCTCCCC 1200
AGGGTTTGC TGGCAATAAA GATGTTGCTG TTGAAG 1236

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1391 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: BRSTNOT04
(B) CLONE: 1969426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120 :

GTACTGCCCA CCACCTCCCT GGGCCACCCC TCACTCAGTG CTCCGGCTCT CTCCTCCTCC 60

PF-0459 US

TCTTCGTCCT CCTCCACTTC ATCTCCTGTT TTGGGCTCCC CCTCTTACCC TGCTTCTTCC 120
CCTGGGGCCT CCCCCCACCA CCGCCGTGTG CCCCTCAGCC CCCTGAGTTT GCTCGCGGGC 180
CCAGCCGACG CCAGAAGGTC CCAACAGCAG CTGCCAAAC AGTTTCGCC ACAATGTCA 240
CCCACCTTGT CTTCCATCAC TCAGGGCGTC CCCCTGGATA CCAGTAAACT GTCCACTGAC 300
CAGCGGTTAC CCCCCATACCC ATACAGCTCC CCAAGTCTGG TTCTGCCTAC CCAGCCCCAC 360
ACCCCCAAAGT CTCTACAGCA GCCAGGGCTG CCCTCTCAGT CTTGTTCACT GCAGTCCTCA 420
GGTGGGCAGC CCCCAGGCAG GCAGTCTCAT TATGGGACAC CGTACCCACC TGGGCCAGT 480
GGGCATGGGC AACAGTCTTA CCACCGGCCA ATGAGTGACT TCAACCTGGG GAATCTGGAG 540
CAGTTCAGCA TGGAGAGCCC ATCAGCCAGC CTGGTGCTGG ATCCCCCTGG CTTTCTGAA 600
GGGCCTGGAT TTTTAGGGGG TGAGGGGCCA ATGGGTGGCC CCCAGGATCC CCACACCTTC 660
AACCACCAGA ACTTGACCCA CTGTTCCCGC CATGGCTCAG GGCCTAACAT CATCCTCACA 720
GGGGACTCCT CTCCAGGTTT CTCTAAGGAG ATTGCAGCAG CCCTGGCCGG AGTGCCTGGC 780
TTTGAGGTGT CAGCAGCTGG ATTGGAGCTA GGGCTTGGGC TAGAAGATGA GCTGCGCATG 840
GAGCCACTGG GCCTGGAAGG GCTAAACATG CTGAGTGACC CCTGTGCCCT GCTGCCTGAT 900
CCTGCTGTGG AGGAGTCATT CCGCAGTGAC CGGCTCCAAT GAGGGCACCT CATCACCATC 960
CCTCTCTTG GCCCCATCCC CCACCACCAT TCCTTCCCTC CCTTCCCCCT GGCAGGTAGA 1020
GACTCTACTC TCTGTCCCCA GATCCTCTT CTAGCATGAA TGAAGGATGC CAAGAATGAG 1080
AAAAAGCAAG GGGTTGTCC AGGTGGCCCC TGAATTCTGC GCAAGGGATG GGCCTGGGG 1140
AACTCAAGGG AGGGCCTAAA GCACTTGTAA CTTGAACCG TCTGTCTGGA GGTCAGAGCC 1200
TGTGGAAAG CAGGGTAGA GGGGAGCCCT GGAAGCAGGG CTTTCCGGA TGCCTAGGGG 1260
TGGCAGTGC CAGCCCTCC TCACCACTCT TCCCCTTGCA GTGGAGGAGA GAGCCAGAGT 1320
GGATACTATT TTTTATTAAA TATATTATTA TATGTTAATA AAAAAATCAT ATCAAAAAAA 1380
AAAAAAAAG G 1391

(2) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2183 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: UCMCL5T01
 - (B) CLONE: 1969948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121 :

CTCTGTGAAC ATATGATGAG AGAAGCCAAG ATCATGCAGT ATAAGTACCT ACTGTTCACT 60
CTTCACGCCA TAGTGAAGCT TGGAAATCCCT CAGAACACTA TTTTGGTGCA GACTTTGCTG 120
AGGGTGACCC AGGAACGTAT CAATGAGTGT GATGAGATAT GCCTTCAGT TTTGTCAACT 180
GTTTAGAGG CAATGGAACC ATGCAAGAAT GTTCATGTTAC TACGAACGGG ATTCAAGAATA 240
CTAGTTGATC AGCAAGTTG GAAAATAGAA GATGTCTTCA CATTACAAGT TGTGATGAAG 300
TGTATTGGAA AAGATGCACC GATTGCTCTT AAGAGGAAAC TGGAGATGAA AGCCTTGAGG 360
GGATTAGACA GATTTCTGT TTTGAATAGC CAACACATGT TTGAAGTACT AGCTGCCATG 420
AATCACCGAT CTCTTATACT CCTGGATGAA TGCAGTAAGG TGGTCCTAGA TAATATCCAT 480
GGGTGTCCTT TAAGAATAAT GATCAACATA TTGCAGTCCT GCAAAGACCT CCAGTACCAT 540
AATTGGATC TCTTCAAGGG ACTTGCAGAT TATGTGGCTG CAACTTCGA CATCTGGAAG 600
TTCAGAAAAG TTCTTTTAT CCTCATTAA TTTGAAAACC TTGGCTTCG ACCTGTTGGT 660
TTAATGGACC TGTTATGAA GAGAATAGTA GAGGATCCTG AATCCCTAAA CATGAAAAAC 720
ATTCTATCTA TTCTTCATAC TTACTCTTCT CTCAATCATG TCTACAAATG CCAGAACAAA 780
GAACAGTTCG TGGAAGTTAT GGCTAGTGCT CTGACTGGTT ATCTTCACAC TATTCTTCT 840
GAAAACCTAT TGGATGCAGT ATATTCAATT TGCTTGATGA ATTACTTCC CCTGGCTCCT 900
TTAATCAGC TTCTGCAAAA AGACATCATC AGTGAGCTGC TGACATCAGA TGACATGAAG 960
AATGCTTACA AGCTGCATAC TTTGGATACT TGTCTAAAAC TTGATGATAC TGTCTATCTG 1020
AGGGACATAG CCTTGTCACT CCCACAGCTG CCGCGGGAGC TGCCATCGTC ACATACAAAT 1080
GCAAAGGTGG CAGAGGTGCT GAGCAGCCTT CTGGGAGGTG AAGGACACTT CTCAAAGGAT 1140
GTGCACTTGC CACACAATTAA TCATATTGAT TTTGAAATCA GAATGGACAC TAACAGGAAT 1200
CAAGTGCTAC CACTTCTGA TGTGGATACA ACTTCTGCTA CAGATATTCA AAGAGTAGCT 1260
GTGCTATGTG TTTCCAGATC TGCTTATTGT TTGGGTTCAA GCCACCCAG AGGATTCCCTT 1320
GCTATGAAAA TGCAGCATTAA GAATGCAATG GGTTTCATG TGATCTGGT CAATAACTGG 1380
GAGATGGACA AACTAGAGAT GGAAGATGCA GTCACATTAA TGAAGACTAA AATCTATTCA 1440
GTAGAAGCTC TTCTGTTGC TGCTGTAAAT GTGCAAAGCA CACAATAAG TGAAAATCAA 1500
CCTTTCTATA TTAGGAGACA TGCATTTGTA AAAATTAATA AAGATGACAA GTCAGTTGTC 1560
AATGGAATTG AGCTATCTGC TAAGACAAAA AATGTTACCT CAGTTCACTA TTAAAATTAA 1620
TTTTAGGAGT GGAAGAAATG TTGTTACTGC CATTAAAAAA TATGCTGAGA AAATTCCAGA 1680
AGGGTTATTAA TTCCAACCAC ACCTATTCCC TCTAGTGCCC AGATATTGA TTTGTGAGCT 1740
GTACGTTCA CCTTTCTATC TTTGATCTAC TAAAAACTGG TTTCTTAGTT GTGAGGTGTC 1800

ACAGGCAGGT TGATGTGGGT AGTAGTCCTT GTCTTGAA TCTGAATATT TATACTCCTG 1860
 CTCTAAGCTG TTCTAAGACT TGGGGTTATG CCTTTAAATC ATTTCAAGC ATTGGCCAAA 1920
 TAATAATTGG ACAAAAGTTCT AAAGTTGTCA AGTGTGTAAG AATTAGTGAG GTAGCTGTTG 1980
 AAAATGAGTG AGGATGGTAT TTGTATTGT AATAAGCACT GCAGGTAGAG ATATTCATG 2040
 GGTTATAATA AGAGAAACAC AGATGAGATG TAGATGGTAA GGAGTCTTAC TGTTGTTGG 2100
 GTCCTTCCTT TCTCTTCTT TTTTCCCCCT TACCCCTCCC ACAATTTCAT GAAGTCTTT 2160
 AAATTAAATA TATAGCTTNA ATT 2183

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2066 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: LUNGAST01
 (B) CLONE: 1988911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122 :

AGAACCACTG CAGTGGAGAC TCCATGTGCA AAAGAAAAAA ACCAAATGTG AGTCATAAA 60
 GACTTTCTGC CAGCATGTGG GTGACATTGT TTCTTGCAAG ATTTGGCTA TGGAAAGGG 120
 AAATGTTCTA AGCAGAGCCC CGTCAAGAGC CCACGGGACA CATTGGAG ATGACAGATT 180
 TGAAGATCTG GAAGAGGCAA ATCCATTCTC TTTAGAGAG TTTCTGAAGA CCAAGAACCT 240
 CGGCCTCTCG AAAGAGGATC CGGCCAGCAG AATTATGCA AAGGAAGCCT CGAGGCATTC 300
 CCTGGGACTT GACCACAACT CCCCACCCCTC CCAAACCGGC GGGTATGGCC TGGAGTATCA 360
 GCAGCCATT TTGAGGATC CGACAGGGGC TGGTGACCTC CTGGATGAGG AGGAGGATGA 420
 GGACACCGGA TGGAGTGGGG CCTACCTGCC GTCCGCCATC GAGCAGACTC ACCCCGAGAG 480
 GGTCCCTGCC GGCACGTCGC CCTGCAGCAC ATACCTTCC TTTTCTCCA CCCCCTCGGA 540
 GCTGGCAGGG CCTGAGTCTC TGCCCTCGTG GGCAGTGGAGT GACACTGATT CTCGCGTGT 600
 TCCGGCCTCT CCGGCAGGGA GTCCTAGCGC AGACTTGCG GTTCATGGAG AGTCTCTGGG 660
 AGACAGGCAC CTGCGGACGC TGCAAGATAAG TTACGACGCA CTGAAAGATG AAAATTCTAA 720
 GCTGAGAAGA AAGCTGAATG AGGTTCAGAG CTTCTCTGAA GCTCAAACAG AAATGGTGAG 780
 GACGCTTGAG CGGAAGTTAG AAGCAAAAT GATCAAGGAG GAAAGCGACT ACCACGACCT 840
 GGAGTCGGTG GTTCAGCAGG TGGAGCAGAA CCTGGAGCTG ATGACCAAAC GGGCTGTAAA 900

PF-0459 US

GGCAGAAAAC CACGTCGTGA AACTAAAACA GGAAATCACT TTGCTCCAGG CGCAGGTCTC 960
CAACTTCCAG CGAGAGAATG AAGCCCTGCG GTGCCGCCAG GGTGCCAGCC TGACCGTGGT 1020
GAAGCAGAAC GCCGACGTGG CCCTGCAGAA CCTCCGGGTG GTCATGAACA GTGCACAGGC 1080
TTCCATCAAG CAACTGGTTT CCGGAGCTGA GACACTGAAT CTTGTTGCCG AAATCCTTAA 1140
ATCTATAGAC AGAATTCTG AAGTTAAAGA CGAGGAGGAA GACTCTTGAG GACCCCTGGG 1200
TGTTCTCAGC ATGAAGCTCC GTGTATAACCC TGAGGTCACC ACCGCTCGAT CTAAATGTGC 1260
AGTTGTGTCC TTAAATATGC AGTCTTCACC CAGAGTAAAG TGTTGATCGC AAGAGTCCAG 1320
TGTCGTGCCCG TCAGCCAGTT CTTGGCCACC ACAATGGGAG CAGCCCTGGC CGAGTTGTCT 1380
CTGTGGTTTC TATGCAGCCC TTCTGGCGA AATTCCTGCG ATCTTATAGA TTCTAATGAG 1440
CTCTTGGAAAG ACATTGTCAT AAAAGCCAGT GATTTAAGA AAAAGAGTGG TTCTGGAATC 1500
AATGTTTCC AGTCCCATCC CAGAACATCA GTTGTAAAGAT AAGTACAATT GGTTGTCCCT 1560
GATTCATAA GTAGAACAAA CACTAAATGT GCCTCTGAGA TGGCCACCCCC GGGCAGGGAC 1620
CTGTGCCTTC CGCCGATGCT CAGGGCTCCC TCTGGCTCCC GGGTCACTCT TGTGGCCCCA 1680
GTGGGTGGTC CCTGCAGTCA TGGCCTGAGT GCGCAGGGGC CACCGCGTGG CTGCTGCTGT 1740
CCTCCTCCGG GACCCACGGG GACCAAGGTC ACACGTTCCG TGCTGTGAAG CTGTCCAGAT 1800
GTGCCTCTT GGCTGGGGT TCTGGTGGAC GTTCAAGTG GCATTTGTA CAATGCAGGT 1860
TAGAATTCAAG GAATTCAAG TATGTGCCCG GGTCTGTCAG GTCCCAGTTG CTTTCTGAC 1920
GGCCCCCCTC AGAGGGACGG CGATGAGCAC TAAATGCTTT TTTGACTATT TTCCTATAGA 1980
TTTTTTTAA AACTTTTTT TCCTCCTGTT CCAATTGATA GCTTTCTTAT TTAATAAATT 2040
CTGTAGTTCA CCGCAAAAAA AAAAAAA 2066

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1867 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: OVARNOT03
(B) CLONE: 2061561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123 :

TGGCCAGGCT GGTCTAGAAC TCCTGACTGC AAATGATCAG CCCGCCTCAG CCACCCAAAG 60
TGTTGGGATT ACAGGGTGTGA GCCACTGTGC CCAGCGTGAT TTTTTTTTT TTTAAAGCAA 120

ACTTGTCCCTT TGGTTTGCA GAACAGGCCT GCTCCCTCTC ATCTAGCCCA TCATTTCTTG 180
 GGGCCTGAAC CCCAGTGGTC CAAAGTATTG CTTGTGAAAT TTAAAAAATG TGAATATGAT 240
 GTGGGGATGG GCCTCTTCTA CATTACCTTG GCCCAGGGGG ATCAGCTGGC TGGGAGGATT 300
 AGTGAGCACC TCTGTATTTT GAGGTCTGAG TCTTCTGGAG CTGTGTAGTT AATCTTCGGT 360
 TTCTGATAAC CCCTGGGTCC ATCTGGCCAT CAGCCTCAGC AGTGAGCAAA GCAATACCAT 420
 ACTCATTCT ATGTTCCCTGT TCCTTCCTCT GCTCCTCCTT TGGAGAAGCA ATAATTGATG 480
 GGGGATGATA CAGTAGCACT TTACAAATGG CTCCATGTCA TTCATCCCAG GGGCCATAAT 540
 CTCTTGCACC ACCTATTCTT ACTTCCTGTT CAGCTCCTT ACAGCTTTA TTTTCAACTG 600
 CCTCCCAACT TGGTGGGCC TCCTTTAAGG ATGAGCCAAT AGTAAGAATG TGGCTGTAAT 660
 CAGCAGAGAC CCCTCTGAGG GGTATCTGTT CTGCAGCCCC TAGTGAAATC ATGTGATGTG 720
 AGACAGAAAC CTAAACATGG TACTTGATTC TAAACCTGTG CCAGTCTATA GCCTCTGCCT 780
 CCCCAAGCAG AGCTCAAGCC AAACGTTCT GTCCTCTTC CTTCTGCATT AACCCCTTG 840
 TGATCCTCAG GGGCCACTCC CCCAACACCC CTGTACTTGG GTGAGGGATG TTGGACAGAG 900
 CCTGTTTCA TGTACTGCAG GTGGGGGTGT GCTGACATGT TTGCTCTTGG TTGATGGAGA 960
 AGGTACAGAG GCCAGGGAGT GAAAATGGTT GACAGAAGAG GGAAGAGTTA GGTGTCTCAT 1020
 AGTCACTCAT AGTGGGGTGG TCAGGGTAA TGGCATCTCC CCACTTCTAGG CTTCTCAAAC 1080
 AGACTTTGA CACCTCTCAA GTTCAGAGCT CTGATGTGGA AAGACAGGAG GTGTGGGAA 1140
 GGAGGGGGAT TTCGTGTGTT TGCATGAGTG TGCCTTCAG GCCTTGGAG TTGGCAAGAG 1200
 GGAGGGGAAGG AAGGAGAGCA AAATCTTCGG AAGGTGTTTC TTGTACCTGA GGGATCCTGC 1260
 CCTGAATCTC CATAGTCTCC ACTGTGAACG GAGGAGGGGA GGGGTGTGCT GGGGAATAAA 1320
 TCTTGTATGA GAACAATCAA AAATCAAACG AATCCCACCG ACAGACTGCT GCTCCTAGTG 1380
 ATCTGGACTC ACCTAGGGGG CATCTGGCT GGGGTTCCAN GCTTACGTNC GCGTGNATGN 1440
 GACGN CANAG CTCTTCGAAA GTGTCCCNA AANTNCAATTG ATTGGCGGTG GTTTAAAAG 1500
 TTCGGGCCTG GGAAACCCGG GGGNTTACCC ATTTTATCCC NCTTNGANGG CANATTCCCC 1560
 TTTTCCCCA ATTTGGGAA ATTNCCAAA NGGGNCCCGT AACGGTTGGC CTTTCCCAA 1620
 AATTNGGNC GCCCTTAATT GGGCGATTG TGGGACCCGC GCCCTTATA GGGGGGGGCT 1680
 TTAAAGCGGC GCNGGGGTT CTTTGGGTGA TTACCGGCAGC GGTTGACCCC GGGTAAAATA 1740
 TTGACAAGGG CCCTTAGCG CGCGGTTCCCT TGTGGGGTTT TCCTCCCATT TGCTTTTCC 1800
 GCAAAAGTTT TGGCGGGGTT TTCCCCGGAA AAGGTCTAA AAAGCGGTGT GCCCCTCTTT 1860
 GAGGGGG 1867

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PANCNOT04
- (B) CLONE: 2084489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124 :

CTCTGGGTCT GTAGCAACCG CCCAGCGTTG AGGCGCGGCT CATGCCCTCA GTATCCCGGT 60
 CCAGCTATTG CGAGGACATC GTGGGCTCTC GGAGAAGGCG ACGCAGCTCC TCGGGGAGCC 120
 CACCATCCCC GCAGAGCAGA TGTCCTCTT GGGATGGCTG TTCCCGCTCT CACTCCCGCG 180
 GCCGTGAGGG CCTCAGGCCT CCTTGGAGTG AGTTGGACGT GGGCGCTCTT TACCCCTTA 240
 GTCGCTCTGG GTCGCGAGGG CGGCTCCAA GATTCCGCAA CTACGCCCTC GCGTCCTCCT 300
 GGTCGACCTC GTATAGTGGA TATCGCTACC ATCGTCACTG CTATGCAGAA GAACGGCAGT 360
 CAGCGGAAGA CTACCGAGAAG GAAGAGAGCC ATCGGCAGAG GAGGCTGAAG GAGAGAGAGA 420
 GGATTGGGGA ATTGGGAGCG CCTGAAGTGT GGGGGCCGTC TCCAAAGTTC CCTCAGCTAG 480
 ATTCTGACGA ACATAACCCCA GTTGAGGATG AAGAAGAGGT AACGCATCAG AAAAGCAGCA 540
 GTTCAGATTG CAACTCGGAA GAACATAGGA AAAAGAAGAC CAGTCGTTCA AGAAACAAGA 600
 AAAAAAAGAAA GAATAAGTCG TCTAAAAGAA AGCATAGGAA ATATTCTGAT AGTGACAGTA 660
 ACTCAGAGTC TGACACAAAT TCTGACTCTG ATGATGATAA AAAGAGAGTT AAAGCCAAGA 720
 AGAAAAAAGAA GAAAAAAGAAA CACAAAACAA AGAAAAAAGAA GAATAAGAAA ACCAAAAAAG 780
 AATCCAGTGA CTCAAGCTGT AAAGACTCAG AAGAGGACTT GTCAGAAGCT ACCTGGATGG 840
 AGCAGCCAAA TGTGGCAGAT ACTATGGATT TAATAGGGCC AGAAGCACCT ATAATACATA 900
 CCTCTCAAGA TGAAAAACCT TTGAAGTATG GCCATGCTT GCTTCCCGGT GAAGGTGCAG 960
 CTATGGCTGA GTATGTAAAA GCTGGAAAGC GAATCCCACG AAGAGGTGAA ATTGGGTTGA 1020
 CAAGTGAAGA GATCGGTTCT TTTGAATGCT CAGGTTATGT CATGAGTGGT AGCAGGCATC 1080
 GCAGAATGGA GGCTGTACGA CTGCGTAAGG AGAACCAAGAT CTACAGTGCT GATGAGAAGA 1140
 GAGCTCTTGC ATCCTTAAAC CAAGAAGAGA GACGAAAGAG AGAAAGTAAG ATTTTAGCCA 1200
 GTTCCGAGA GATGGTGCAC AAAAAGACAA AAGAGAAAGA TGACAAGTAA GGACTTACTT 1260
 GTTGCACAGC AGGAATTTA ACAACAAAAA TTTTATGTGA CCAAAAGTGT TAAAAGGCTT 1320
 TACAGTGCTA CTGTACTTAC CATATTAGTA AGTCCCTCAG GAAAAAGCTT CTTTGAGAT 1380

ATCTTTAGCA GCTTATTTT TGTTATTTA ACTTTAAAAA GTAATATGTG CACATGGTTT 1440
TAAAAATATT CAACCATTAT AGGAGGAGAG TTAGTAAAAA GTGAATCTT CACTTAGCC 1500
CCTGACACCT TTCCCCAAA AATATATATT TTGGTGTCTT ATATACAGAA TATACATTCT 1560
GTGCATATAC AAGAGTATAT GTTGCAGCAT AAAGATTAAA AGCTATTAAA GTTTTTTTC 1620
GCTCGTTA 1628

(2) INFORMATION FOR SEQ ID NO: 125:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: SPLNFET02
(B) CLONE: 2203226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125 :

GTGGCGGCCG CGAAGGATGC ACCCGGCAGG CTTGGCGGCG GCGGCTGCGG GGACGCCCG 60
GCTGCCCTCG AAGCGGAGGA TCCCTGTGTC CCAGCCGGC ATGGCCGACC CCCACCAGCT 120
TTTCGATGAC ACAAGTTCA G CCCAGAGCCG GGGCTATGGG GCCCAGCGGG CACCTGGTGG 180
CCTGAGTTAT CCTGCAGCCT CTCCCACGCC CCATGCAGCC TTCCTGGCTG ACCCGGTGTC 240
CAACATGGCC ATGGCCTATG GGAGCAGCCT GGCGCGCAG GGCAAGGAGC TGGTGGATAA 300
AACATCGAC CGCTTCATCC CCATCACCAA GCTCAAGTAT TACTTGCTG TGGACACCAT 360
GTATGTGGC AGAAAGCTGG GCCTGCTGTT CTTCCCTAC CTACACCAGG ACTGGGAAGT 420
GCAGTACCAA CAGGACACCC CGGTGGCCCG CCGCTTGAC GTCAATGCC CGGACCTCTA 480
CATTCCAGCA ATGGCTTCA TCACCTACGT TTTGGTGGCT GGTCTTGCAG TGGGGACCCA 540
GGATAGGTTTC TCCCCAGACC TCCTGGGGCT GCAAGCGAGC TCAGCCCTGG CCTGGCTGAC 600
CCTGGAGGTG CTGGCCATCC TGCTCAGCCT CTATCTGGTC ACTGTCAACA CCGACCTCAC 660
CACCATCGAC CTGGTGGCCT TCTTGGGCTA CAAATATGTC GGGATGATTG GCAGGGTCCT 720
CATGGGCCTG CTCTTCGGGA AGATTGGCTA CTACCTGGTG CTGGGCTGGT GCTGCGTGGC 780
CATCTTGTG TTCAATGATCC GGACGCTGCG GCTGAAGATC TTGGCAGACG CAGCAGCTGA 840
GGGGGTCCCG GTGCGTGGGG CCCGGAACCA GCTGCGCATG TACCTGACCA TGGCGGTGGC 900
GGCGCGCAG CCTATGCTCA TGTACTGGCT CACCTCCAC CTGGTGCAGT GAGCGCGCCC 960
GCTGAACCTC CCGCTGCTGC TGCTGCTGCT GGGGGCCACT GTGGCCGCCG AACTCATCTC 1020

CTGCCTGCAG GCCCCAAGGT CCACCCCTGTC TGGCCACAGG CACCGCCTCC ATCCCATGTC 1080
CCGCCAGCC CGCCCCCAA CCCAAGGTGC TGAGAGATCT CCAGCTGCAC AGGCCACCGC 1140
CCCAGGGCGT GGCGCTGTT ACAGAAACAA TAAACCTGA TGGGCATGGC AAAAAAAA 1200

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1093 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: PROSNOT16
(B) CLONE: 2232884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126 :

AGAGCCCCAG CCACGCCGGC CCAGGTGGCC TCAGGTGAGG GGGGGCGGAC GCACCTGTGG 60
GGACGGGACG ACGAGTTCAA GCCTCCGTGG GTGCAGTTGG TCGCCAGCGA GGGATGCGGA 120
GACGCCCTG AACGACCATG GCATCGGCCG ACGAGCTGAC CTTCCATGAA TTCGAGGAGG 180
CCACTAATCT TCTGGCTGAC ACCCCAGATG CAGCCACCAC CAGCAGAAC GATCAGCTGA 240
CCCCACAAGG GCACGTGGCT GTGGCCGTGG GCTCAGGTGG CAGCTATGGA GCCGAGGATG 300
AGGTGGAGGA GGAGAGTGAC AAGGCCCGC TCCTGCAGGA GCAGCAGCAG CAGCAGCAGC 360
CGGGATTCTG GACCTTCAGC TACTATCAGA GCTTCTTGA CGTGGACACC TCACAGGTCC 420
TGGACCGGAT CAAAGGCTCA CTGCTGCCCG GGCCTGGCCA CAACTTGTG CGGCACCAC 480
TGCAGGATCG GCCGGATCTG TATGGCCCT TCTGGATCTG TGCCACGTTG GCCTTGTCC 540
TGGCCGTAC TGGCAACCTG ACGCTGGTGC TGGCCAGAG GAGGGACCCC TCCATCCACT 600
ACAGCCCCCA GTTCCACAAG GTGACCGTGG CAGGCATCAG CATCTACTGC TATGCGTGGC 660
TGGTGGCCCT GGCCCTGTGG GGCTTCCTGC GGTGGCGCAA GGGTGTCCAG GAGCGCATGG 720
GGCCCTACAC CTTCCCTGGAG ACTGTGTGCA TCTACGGCTA CTCCCTCTT GTCTTCATCC 780
CCATGGTGGT CCTGTGGCTC ATCCCTGTGC CTTGGCTGCA GTGGCTCTT GGGCGCTGG 840
CCCTGGGCCT GTCAGCCGCC GGGCTGGTAT TCACCCCTCTG GCCCGTGGTC CGTGAGGACA 900
CCAGGCTGGT GGCCACAGTG CTGCTGTCCG TGGTCGTGCT GCTCCACGCC CTCCTGGCCA 960
TGGGCTGTAA GTTGTACTTC TTCCAGTCGC TGCCTCCGGA GAACGTGGCT CCTCCACCCC 1020
AAATCACATC TCTGCCCTCA AACATCGCGC TGTCCCTAC CTTGCCGCAG TCCCTGGCCC 1080
CCTCCTAGGA AGG 1093

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNOT11
- (B) CLONE: 2328134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127 :

GCAGGGGGATG ACGCCACGGA CATGGTGGCC GAGACCGGCG GGGTGGGGGA CGTGTGCGGC 60
GGCCGGGTGG CCTCGGTGG TACCCTGGGC GCGGACAGCT GCCTCATTAG TATTCGTACC 120
CACGAGGCAGG CGCAGCGGGC CCTCGGGGAC AGCGAGCGTC GCGGCTATGG CTTATCACTC 180
GGGCTACGGA GCCCACGGCT CCAAGCACAG GGCCCAGGCA GCCCCGGATC CCCCTCCCCT 240
CTTCGATGAC ACAAGCGGTG GTTATTCCAG CCAGCCCGGG GGATACCCAG CCACAGGAGC 300
AGACGTGGCC TTCAGTGTCA ACCACTTGCT TGGGGACCCA ATGGCCAATG TGGCTATGGC 360
CTATGGCAGC TCCATCGCAT CCCATGGGAA GGACATGGTG CACAAGGAGC TGCACCGTTT 420
TGTGTCTGTG AGCAAACCTCA AGTATTTTT TGCTGTGGAC ACAGCCTACG TGGCCAAGAA 480
GCTAGGGCTG CTGGTCTTCC CCTACACACA CCAGAACTGG GAAGTGCAGT ACAGTCGTGA 540
TGCTCCTCTG CCCCCCCGGC AAGACCTCAA CGCCCTGAC CTCTATATCC CCACGATGGC 600
CTTCATTACT TACGTGCTCC TGGCTGGGAT GGCACGGGAT ATTCAAGAAAA GGTTCTCCCC 660
GGAGGTGCTG GGCCTGTGTG CAAGCACAGC GCTGGTGTGG GTGGTGATGG AGGTGCTGGC 720
CCTGCTCCTG GGCCTCTACC TGGCCACCGT GCGCAGTGAC CTGAGCACCT TTCACCTGCT 780
GGCCTACAGT GGCTACAAAT ACGTGGGAAT GATCCTCAGT GTGCTCACGG GGCTGCTGTT 840
CGGCAGCGAT GGCTACTACG TGGCGCTGGC CTGGACCTCA TCGGCGCTCA TGTACTTCAT 900
TGTGCGCTCT TTGCGGACAG CAGCCCTGGG CCCCCGACAGC ATGGGGGGCC CCGTCCCCCG 960
GCAGCGTCTC CAGCTCTACC TGACTCTGGG AGCTGCAGCC TTCCAGCCCC TCATCATATA 1020
CTGGCTGACT TTCCACCTGG TCCGGTGACC CCCTGGCCCC AGATGGCACT GAGTTTTCA 1080
TTCATTGAAG ATTTGATTTC CTTGAAAAAA AAAAAAAAAG G 1121

(2) INFORMATION FOR SEQ ID NO: 128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1861 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: ISLTNOT01
 - (B) CLONE: 2382718

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128 :

CGCGGACTGT GTCTGTTCCC AGGAGTCCTT CGGCGGCTGT TGTGTCAGTG GCCTGATCGC 60
 GATGGGGACA AAGGCGCAAG TCGAGAGGAA ACTGTTGTGC CTCTTCATAT TGGCGATCCT 120
 GTTGTGCTCC CTGGCATTGG GCAGTGTAC AGTGCACCTCT TCTGAACCTG AAGTCAGAAT 180
 TCCTGAGAAT AATCCTGTGA AGTTGTCTG TGCCTACTCG GGCTTTCTT CTCCCCGTGT 240
 GGAGTGGAAAG TTTGACCAAG GAGACACCCAC CAGACTCGTT TGCTATAATA ACAAGATCAC 300
 AGCTTCCTAT GAGGACCGGG TGACCTTCTT GCCAACTGGT ATCACCTTCA AGTCCGTGAC 360
 ACGGGAAGAC ACTGGGACAT ACACTTGTAT GGTCTCTGAG GAAGGCGGCA ACAGCTATGG 420
 GGAGGTCAAG GTCAAGCTCA TCGTGCTTGT GCCTCCATCC AAGCCTACAG TTAACATCCC 480
 CTCCCTTGCC ACCATTGGGA ACCGGGCAGT GCTGACATGC TCAGAACAAAG ATGGTTCCCC 540
 ACCTTCTGAA TACACCTGGT TCAAAGATGG GATACTGATG CCTACGAATC CCAAAGCAC 600
 CCGTGCCTTC AGCAACTCTT CCTATGTCCT GAATCCCACA ACAGGAGAGC TGGTCTTGA 660
 TCCCCGTCA GCCTCTGATA CTGGAGATA CAGCTGTGAG GCACGGAATG GGTATGGAC 720
 ACCCATGACT TCAAATGCTG TGCGCATGGA AGCTGTGGAG CGGAATGTGG GGGTCATCGT 780
 GGCAGCCGTC CTTGTAACCC TGATTCTCCT GGGAAATCTTG GTTTTGGCA TCTGGTTTGC 840
 CTATAGCCGA GGCCACTTTG ACAGAACAAA GAAAGGGACT TCGAGTAAGA AGGTGATTAA 900
 CAGCCAGCCT AGTCCCCGAA GTGAAGGAGA ATTCAAACAG ACCTCGTCAT TCCTGGTGTG 960
 AGCCTGGTCG GCTCACCGCC TATCATCTGC ATTTGCCTTA CTCAGGTGCT ACCGGACTCT 1020
 GGCCCCTGAT GTCTGTAGTT TCACAGGATG CCTTATTGT CTTCTACACC CCACAGGGCC 1080
 CCCTACTTCT TCGGATGTGT TTTTAATAAT GTCAGCTATG TGCCCCATCC TCCTTCATGC 1140
 CCTCCCTCCC TTTCCTACCA CTGCTGAGTG GCCTGGAACCT TGTTAAAGT GTTTATTCCC 1200
 CATTCTTTG AGGGATCAGG AAGGAATCCT GGGTATGCCA TTGACTTCCC TTCTAAGTAG 1260
 ACAGCAAAAA TGGCGGGGGT CGCAGGAATC TGCACCAAC TGCCCACCTG GCTGGCAGGG 1320
 ATCTTTGAAT AGGTATCTTG AGCTTGGTTC TGGGCTCTT CCTTGTGTAC TGACGACCAG 1380
 GGCCAGCTGT TCTAGAGCGG GAATTAGAGG CTAGAGCGGC TGAAATGGTT GTTTGGTGT 1440
 GACACTGGGG TCCTTCCATC TCTGGGGCCC ACTCTTTCT GTCTTCCCAT GGGAAAGTGCC 1500

PF-0459 US

ACTGGGATCC CTCTGCCCTG TCCTCCTGAA TACAAGCTGA CTGACATTGA CTGTGTCTGT 1560
GGAAAATGGG AGCTCTTGTGTT GTGGAGAGCA TAGTAAATTT TCAGAGAACT TGAAGCCAAA 1620
AGGATTAAA ACCGCTGCTC TAAAGAAAAG AAAACTGGAG GCTGGCGCA GTGGCTCACG 1680
CCTATAATCC CAGAGGCTGA GGCAGGCGGA TCACCTGAGG TCGGGAGTTC GGGATCAGCC 1740
TGACCAACAT GGAGAAACCC TACTGAGAAT ACAAAAGTTAG CCAGGCATGG TGGTGCATGC 1800
CTGTAATCCC AGCTGCTCAG GAGCCTGGCA ACAAGAGCAA AACTCCAGCT CAAAAAAA 1860
A 1861

(2) INFORMATION FOR SEQ ID NO: 129:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1975 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: ENDANOT01
(B) CLONE: 2452208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129 :

GTTTGGAGGA GACTCGGATA TACCTTCTCA GAAGCTGCAC AGGAGGAAAG CAGTGACAAA 60
GAAAGAAGTT GTCATTCTTT GCACGAAACT GGATGGCTTC TACAGGGAGC CAGGCCTCTG 120
ATATAGACGA GATTTTGGA TTCTTCAACG ATGGCGAACCC TCCCACCAAA AAGCCCAGGA 180
AGCTGCTTCC AAGCTTAAAA ACTAAGAAGC CTCGAGAAGT TGTGCTAGTG ATTGGAACAG 240
GCATTAGTGC TGCAGTTGCG CCCCAAGTTC CAGCCCTCAA ATCCTGGAAG GGGTTAACATC 300
AGGCCTTACT GGATGCTGCC ATTGATTTG ATCTTTAGA AGATGAGGAG AGCAAAAAGT 360
TTCAGAAATG TCTCCATGAA GACAAGAACCC TGGTCATGT TGCCCATGAC CTTATCCAGA 420
AACTCTCTCC TCGTACCAAGT AATGTTCGAT CCACATTTT CAAGGACTGT TTATATGAAG 480
TATTTGATGA CTTGGAGTCA AAGATGGAAG ATTCTGGAAA ACAGCTACTT CAGTCAGTTC 540
TCCACCTGAT GGAAAATGGA GCCCTCGTAT TAACTACAAA TTTTGATAAT CTCTTGGAAC 600
TGTATGCAGC AGATCAGGGG AAACAGCTTG AATCCCTGAA CCTTACTGAT GAGAAAAGG 660
TCCTCGAGTG GGCTCAGGAG AAGCGTAAGC TGAGCGTGTGTT GCATATTACAC GGAGTCTACA 720
CCAACCCTAG TGGCATTGTC CTTCATCCGG CTGGATATCA GAACGTGCTC AGGAACACTG 780
AAGTCATGAG AGAAATTCAG AACTCTACG AAAACAAGTC ATTTCTTTTC CTGGGCTGTG 840
GCTGGACTGT GGATGACACC ACTTTCCAGG CCCTTTCTT GGAGGCTGTC AAGCATAAAT 900

CTGACCTAGA ACATTCATG CTGGTCGGA GAGGAGACGT AGATGAGTTC AAAAAGCTTC 960
 GAGAAAACAT GCTGGACAAG GGGATTAAAG TCATCTCCTA TGGAGATGAC TATGCCGATC 1020
 TTCCAGAATA TTTCAAGCGA CTGACATGTG AGATCTCCAC AAGGGGTACA TCAGCAGGGA 1080
 TGGTGAGAGA AGGTCAAGCTA AATGGCTCAT CTGCAGCACA CAGTGAAATA AGAGGCTGTA 1140
 GTACATGAGC GAGCTAGAGA AATCACCAACC GTTAGACCA AGCTGTAAGG CCCTACTACA 1200
 GACAGTGTGTT AACAAAGTAAA CTTACAAGAA CCCAACACAA TTCCAGAGAA GTAACAATAG 1260
 CCAGAGGTTG AAGGGCGGGG TAGAAGAGGG GGGAAATGTTG CAGCGTAATC CTTCATACCA 1320
 CCTGGTTCTT GATATTCTGC CGCCTGTTCA AGTTCAAGAA TAAAAGCGAC AGCAGGACCC 1380
 AAATGCAGCT CCCAACCCAC TCCCCAGGCT AGACATGCTT GTGTCCACAC AGCACACCAA 1440
 TGTGATACTT CCACTGACCG GCTGCAGCTC TGCACTGAAGG ACTCGGGTC TGGATGCCAT 1500
 GGAATCACTG TGGCTCTTGT TGCAGTTTG TACTCTATAC TTGGTTTTTC AATTAAGCTT 1560
 AATGGCTTTT TTAAAACATG ACTTGAAAGCT CTAGTTTCT AGATCTTTA CAGTGTACAG 1620
 TATTTTACAT AACTAAGCTG TATTAAAAGC TTGTTCATTT ACTTGCCAGG ACCCTGGCTC 1680
 TACTTTAGA GTCATTGTAA GAAACTCTAA CTTGCATCAA GGTACTAATA AGCTTAATT 1740
 TAATAACCCA AAGTTAAAG GTTCCGATCT TTCTCCTTGG GGTGGAGTGA TCTCATTCTC 1800
 AGGACAACCG TTTACTTACC TGATTCTCG GAGCATTATC AACTCTGCT CTGTTGTCC 1860
 GACCATACAT ATGTCCTAGA ACTACAGTTA AGTGTGTTGT GGAATTTAG TTTGAATCC 1920
 GGAATAAATG AAGTCCCAGG ACTCAAAGAA GAGAGAAAAA AAAAAAGGGG GCCCC. 1975

(2) INFORMATION FOR SEQ ID NO: 130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2160 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: ENDANOT01
 - (B) CLONE: 2457825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130 :

TCTACTGTCC CCTGCCCTGT ACCCCCAGGC ATTGATCTGG AGAACATTGT GTACTACAAG 60
 GACGACACCC ACTACTTGT GATGACAGCC AAGAACAGT GCCTGCTGCG GCTGGGGGTG 120
 CTGCGCCAGG ACTGCCAGA CACCAATCGG CTGCTGGCA GTGCCAATGT GGTGCCGAG 180
 GCTCTGCAGC GCTTACCCG GGCAGCTGCT GACTTGCCA CCCATGGCAA GCTCGGGAAA 240

CTAGAGTTG CCCAGGGATGC CCATGGGCAG CCTGATGTCT CTGCCTTGA CTTCACGAGC 300
ATGATGCGGG CAGAGAGTTC TGCTCGTGTG CAAGAGAAGC ATGGCGCCCG CCTGCTGCTG 360
GGACTGGTGG GGGACTGCCT GGTGGAGCCC TTCTGGCCCC TGGGCACTGG AGTGGCACGG 420
GGCTTCCTGG CAGCCTTGA TGCAGCCTGG ATGGTGAAGC GGTGGGCAGA GGGCGCTGAG 480
TCCCTAGAGG TGTTGGCTGA GCGTGAGAGC CTGTACCAAGC TTCTGTCACA GACATCCCCA 540
GAAAACATGC ATCGCAATGT GGCCCAGTAT GGGCTGGACC CAGCCACCCG CTACCCCAAC 600
CTGAACCTCC GGGCAGTGAC CCCCAATCAG GTACGAGACCC TGTATGATGT GCTAGCCAAG 660
GAGCCTGTGC AGAGGGACAA CGACAAGACA GATACAGGGG TGCCAGCCAC CGGGTCGGCA 720
GGCACCCAGG AGGAGCTGCT ACGCTGGTGC CAGGAGCAGA CAGCTGGTA CCCGGGAGTC 780
CACGTCTCCG ATTTGTCTTC CTCCTGGCT GATGGGCTAG CTCTGTTGC CCTGGTGTAC 840
CGGCTGCAGC CTGGCCTGCT GGAACCCCTCA GAGCTGCAGG GGCTGGGAGC TCTGGAAGCA 900
ACTGCTTGGG CACTAAAGGT GGCAGAGAAT GAGCTGGCA TCACACCGGT GGTGTCTGCA 960
CAGGCCGTGG TAGCAGGGAG TGACCCACTG GGCCTCATTG CCTACCTCAG CCACCTCCAC 1020
AGTGCCTCA AGAGCATGGC CCACAGCCCA GGCCCTGTCA GCCAGGCCTC CCCAGGGACC 1080
TCCAGTGCTG TATTATTCCCT TAGTAAACTT CAGAGGACCC TGCAGCGATC CCGGGCCAAG 1140
GAAAATGCAG AGGATGCTGG TGGCAAGAAG CTGCGCTTGG AGATGGAGGC CGAGACCCCA 1200
AGTACTGAGG TGCCACCTGA CCCAGAGCCT GGTGTACCC TGACACCCCC ATCCCAACAC 1260
CAGGAGGCCG GTGCTGGGA CCTGTGTGCA CTTTGTGGG AACACCTCTA TGTCCTGGAA 1320
CGCCTCTGTG TCAACGGCCA TTTCTTCCAC CGGAGCTGCT TCCGCTGCCA TACCTGTGAG 1380
GCCACACTGT GGCCAGGTGG CTACGAGCAG CACCCAGGCA GTAGAACGTC TCAGTTCTTC 1440
TTCTCAGCTC TTGTGGCCAT GGAGAAGGAG GAAAAAGAGA GTCCCTTCTC CAGTGAAGAG 1500
GAAGAAGAAG ATGTGCCTT GGACTCAGAT GTGGAACAGG CCCTGCAGAC CTTTGCCAAG 1560
ACCTCAGGCA CCATGAATAA CTACCCAACA TGGCGTCGGA CTCTGCTGCG CCGTGCAGAAG 1620
GAGGAGGAGA TGAAGAGGTT CTGCAAGGCC CAGACCATCC AACGGCGACT AAATGAGATT 1680
GAGGCTGCCT TGAGGGAGCT AGAGGCCGAG GGCAGTGAAGC TGGAGCTGGC CTTGAGGCC 1740
CAGAGCAGTT CCCCAGAACCA GCAAAAGAAA CTATGGGTAG GACAGCTGCT ACAGCTCGTT 1800
GACAAGAAAA ACAGCCTGGT GGCTGAGGAG GCCGAGCTCA TGATCACGGT GCAGGAATTG 1860
AATCTGGAGG AGAAACAGTG GCAGCTGGAC CAGGAGCTAC GAGGCTACAT GAACCGGGAA 1920
GAAAACCTAA AGACAGCTGC TGATCGGCAG GCTGAGGAGC AGGTCTGAG GAAGCTGGTG 1980
GATTGGTCA ACCAGAGAGA TGCCCTCATC CGCTTCCAGG AGGAGCGCAG GCTCAGCGAG 2040
CTGGCCTTGG GGACAGGGGC CCAGGGCTAG ACGAGGGTGG GCCGTCTGCT TTCGTTCCA 2100

CAAAGAAAGC ACCTCACCCC AGCACAGTGC CACCCCTGTT CATCTGGGCT GCCTGGCAGA 2160

(2) INFORMATION FOR SEQ ID NO: 131:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 546 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: THP1NOT03
 - (B) CLONE: 2470740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131 :

GAGGAAGAAG AGGAAGAGGG GGCTCCGATT GGGACCCCTA GGGATCCTGG AGATGGTTGT 60
CCTTCCCCCG ACATCCCTCC TGAACCCCT CCAACACACC TGAGGCCCTG CCCTGCCAGC 120
CAGCTCCCTG GACTCCTGTC CCATGGCCTC CTGGCCGGCC TCTCCTTGCG AGTGGGGTCC 180
TCCTCTGGCC TCCTGCCCT CCTGCTGCTG CTGCTGCTTC CATTGCTGGC AGCCCAGGGT 240
GGGGGTGGCC TGCAGGCAGC GCTGCTGGCC CTTGAGGTGG GGCTGGTGGG TCTGGGGGCC 300
TCCTACCTGC TCCTTGTAC AGCCCTGCAC CTGCCCTCCA GTCTTTCCT ACTCCTGGCC 360
CAGGGTACCG CACTGGGGC CGTCCTGGGN CATGAGCTGG CGCCGAAGGC TCATGGGTGT 420
TCCCCTGGGG CTTTGGAACT GCCTGGTTCT TAAGCTTNGG CAAGGCCTAG CTCCAACCTC 480
TGGTGGCTAA TGGCANCCGG GGGGAAANAT GGGTCNGGA AAAAGGGCCC CCGGGTTTCA 540
CCGGGG 546

(2) INFORMATION FOR SEQ ID NO: 132:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 581 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: SMCANOT01
 - (B) CLONE: 2479092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132 :

GCCATGGAGG CCCTGAGGAG GGCCCACGAG GTCGCGCTCC GCCTGCTGCT GTGTAGGCCG 60
TGGGCCTCGC GCGCCGCCGC CCGCCCCAAG CCCAGCGCCT CGGAGGTGCT GACGCGGCAT 120

PF-0459 US

CTGCTGCAGC GGCGCCTGCC GCACTGGACC TCCTTCTGCG TGCCCTACAG CGCCGTCCGC 180
AACGACCAGT TCGGCCTCTC GCACTTCAAC TGGCCGGTGC AGGGGCCAA CTACCACGTC 240
CTGCGCACCG GCTGCTTCCC CTTCATCAAG TACCACTGCT CCAAGGCTCC CTGGCAGGAC 300
CTGGCCCGGC AGAACCGCTT CTTCACGGCG CTCAAGGTCG TCAACCTCGG TATTCCAAGT 360
TTATTATATG GACTTGGCTC CTGGTTATTT GCCAGAGTCA CAGAGACTGT GCATACCAGT 420
TATGGACCCA TAACAGTTA TTTTCTCAAT AAAGAAGATG AAGGTGCCAT GTATTGAAAG 480
TGTGCGTCAA AGAACATAAA TATCAGTGGA TTTTCTCTGT GTATATGTGC AGTATTTATT 540
TTTGATCCTT TAAAATAAAA CTTTGCAAA TAAAAAAA A 581

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1259 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: SMCANOT01
(B) CLONE: 2480544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133 :

GGGCTGGGCC CCGCCGCAGC TCCAGCTGGC CGGCTTGGTC CTGCGGTCCC TTCTCTGGGA 60
GGCCCGACCC CGGCCGCGCC CAGCCCCAC CATGCCACCC GCAGGGCTCC GCCGGGCCGC 120
GCCGCTCACCC GCAATCGCTC TGTTGGTGCT GGGGGCTCCC CTGGTGCTGG CGGGCGAGGA 180
CTGCCTGTGG TACCTGGACC GGAATGGCTC CTGGCATCCG GGGTTAACT GCGAGTTCTT 240
CACCTTCTGC TGCAGGGACCT GCTACCACCG GTACTGCTGC AGGGACCTGA CCTTGCTTAT 300
CACCGAGAGG CAGCAGAACG ACTGCCTGGC CTTCAGCCCC AAGACCATAG CAGGCATCGC 360
CTCAGCTGTG ATCCTCTTTG TTGCTGTGGT TGCCACCACC ATCTGCTGCT TCCTCTGTTC 420
CTGTTGCTAC CTGTACCGCC GGCGCCAGCA GCTCCAGAGC CCATTGAAG GCCAGGAGAT 480
TCCAATGACA GGCATCCCAG TGCAGCCAGT ATACCCATAC CCCCAGGACC CCAAAGCTGG 540
CCCTGCACCC CCACAGCCTG GCTTCATGTA CCCACCTAGT GGTCTGCTC CCCAATATCC 600
ACTCTACCCA GCTGGGCCCC CAGTCTACAA CCCTGCAGCT CCTCCTCCCT ATATGCCACC 660
ACAGCCCTCT TACCCGGGAG CCTGAGGAAC CAGCCATGTC TCTGCTGCC CTTCAAGTGAT 720
GCCAACCTTG GGAGATGCC CTCATCCTGTA CCTGCATCTG GTCCTGGGG TGGCAGGAGT 780
CCTCCAGCCA CCAGGCCCA GACCAAGCCA AGCCCTGGGC CCTACTGGGG ACAGAGCCCC 840

AGGGAAAGTGG AACAGGAGCT GAACTAGAAC TATGAGGGT TGGGGGGAGG GCTTCCAATT 900
ATGGGCTATT TTTACTGGGG GCAAGGGAGG GAGATGACAG CCTGGGTCAC AGTGCCTGTT 960
TTCAAATAGT CCCTCTGCTC CCAAGATCCC AGCCAGGAAG GCTGGGCCCC TACTGTTGT 1020
CCCCTCTGGG CTGGGGTGGG GGGAGGGAGG AGGTTCCGTC AGCAGCTGGC AGTAGCCCTC 1080
CTCTCTGGCT GCCCCACTGG CCACATCTCT GGCTGCTAG ATTAAAGCTG TAAAGACATA 1140
ACTCATATCA GTCGCATCAT TGGACCCATC CACACCTTCC AGGAACACCG NCTTCAGCTG 1200
GGCCCAGACT GTTGCCCACT CCATATTCCA AAAGTAGGGG AGGGCCAGCA CCAGCATCG 1259

(2) INFORMATION FOR SEQ ID NO: 134:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2033 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: BRAITUT21
(B) CLONE: 2518547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134 :

CGGCTCGAGG CCGCAGCCCC ATGGACAGTC TTCTGCACCC CCGGGAGCGC CCTGGATCCA 60
CTGCCTCCGA GAGCTCAGCC TCTCTGGCA GTGAGTGGGA CCTCTCAGAA TCTTCTCTCA 120
GCAACCTGAG TCTTCGCCGT TCCTCAGAGC GCCTCAGTGA CACCCCTGGA TCCTTCCAGT 180
CACCTTCCCT GGAAATTCTG CTGTCCAGCT GCTCCCTGTG CCGTGCCTGT GATTGCTGG 240
TGTATGATGA GGAAATCATG GCTGGCTGGG CACCTGATGA CTCTAACCTC AACACAACCT 300
GCCCTTCTG CGCCTGCCCTT TTTGTGCCCT TGCTCAGTGT CCAGACCCTT GATTCCCGGC 360
CCAGTGTCCC CAGCCCCAAA TCTGCTGGTG CCAGTGGCAG CAAAGATGCT CCTGTCCCTG 420
GTGGTCCTGG CCCTGTGCTC AGTGACCGAA GGCTCTGCCT TGCTCTGGAT GAGCCCAGCT 480
CTGCAACGGG CACATGGGGG GAGCCTCCCG GCGGGTTGAG AGTGGGGCAT GGGCATACCT 540
GAGCCCCCTG GTGCTGCGTA AGGAGCTGGA GTCGCTGGTA GAGAACGAGG GCAGTGAGGT 600
GCTGGCGTTG CCTGAACTC CCTCTGCCCA CCCCCATCATC TTCTGGAACC TTTTGTGGTA 660
TTTCCAACGG CTACGCCCTGC CCAGTATTCT ACCAGGCCTG GTGCTGGCCT CCTGTGATGG 720
GCCTTCGCAC TCCCAGGCCCT CATCTCCTTG GCTAACCCCT GATCCAGCCT CTGTTCAGGT 780
ACGGCTGCTG TGGGATGTAC TGACCCCTGA CCCCAATAGC TGCCCACCTC TCTATGTGCT 840
CTGGAGGGTC CACAGCCAGA TCCCCCAGCG GGTGGTATGG CCAGGCCCTG TACCTGCATC 900

CCTTAGTTG GCACTGTTGG AGTCAGTGCT GCGCCATGTT GGACTCAATG AAGTGCACAA 960
GGCTGTGGGG CTCCTGCTGG AAACTCTAGG GCCCCCACCC ACTGGCCTGC ACCTGCAGAG 1020
GGGAATCTAC CGTGAGATAT TATTCCTGAC AATGGCTGCT CTGGGCAAGG ACCACGTGGA 1080
CATAGTGGCC TTCGATAAGA AGTACAAGTC TGCCTTAAC AAGCTGGCCA GCAGCATGGG 1140
CAAGGAGGAG CTGAGGCACC GGCAGGGCGCA GATGCCCACT CCCAAGGCCA TTGACTGCCG 1200
AAAATGTTT GGAGCACCTC CAGAATGCTA GAGACCTAA GCTTCCTCT CCAGCCTAGG 1260
GTGGGGAAGT GAGGAAGAAG GGATTCTAGA GTTAAACTGC CTCCCTGTTG CCTTCATGGA 1320
GTTGGGAACA GGCTGGGAAG GATGCCAGT CAAAGGCTCC AAGCGAGGAC AACAGGAAGA 1380
GGGATCCACT GTTACCAAAA GTCCTGATTC CCCCATCACC AACCTACCCA GTTGTTCGT 1440
GCTGATGTTG GGGGAGATCT GGGGGGAGTT GGTACAGCTC TGTTCTTCCC TTGTCCTATA 1500
CCGGGAACTC CCCTCCAGGG TACCCACAGA TCTGCATTGC CCTGGTCATT TTAGAAGTTT 1560
TTGTTTAAA AAACAACGG AAAGATGCAG AGCTACTGAG CCTTTGCCCT GAATGGGAGG 1620
TAGGGATGTC ATTCTCCACC AATAATGGTC CCTCTTCCCT GACGTTGCTG AAGGAGCCA 1680
AGGCTCTCCA TGCCTTCTA CCTAAGTGTT TGTATTTAT TTTAAATTAT TTATTCTGGA 1740
GCCACAGCCC CCTTGCTTAT GAGGTTCTTA TGGAGAGTGA GAAAGGGAAG GGAAATAGGG 1800
CACCATGGTC CGGTGGTTG TAGTTCTTC AAAGTCAGGC ACTGGGAGCT AGAGGAGTCT 1860
CAAGCTCCCC TTAGGAAGAA CTGGTGCCCC CTCCAGTCCT AATTTTCTT GCCTGCCCG 1920
CCTTGGGAA TGCCTCACCC ACCCAGGTCC TGACCTGTGC AATAAGGATT GTTCCCTGCG 1980
AAGTTTGTGTT GGATGTAAAT ATAGTAAAG CTGCTTCTGT CTTTTCAAA AAA 2033

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3007 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: GBLANOT02
(B) CLONE: 2530650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135 :

GCCCCACTGGG CTCTCCGGC TGCAGTGCCA GGGCGCAGGA CGCGGCCGAT CTCCCGCTCC 60
CGCCACCTCC GCCACCATGC TGCTCCCCA GCTCTGCTGG CTGCCGCTGC TCGCTGGGCT 120
GCTCCCGCCG GTGCCCGCTC AGAAGTTCTC GGCGCTCACG TTTTGAGAG TGGATCAAGA 180

TAAAGACAAG GATTGTAGCT TGGACTGTGC GGGTCGCC CAGAAACCTC TCTGCGCATC 240
TGACGGAAGG ACCTTCCTTT CCCGTTGTGA ATTTCAACGT GCCAAGTGCA AAGATCCCCA 300
GCTAGAGATT GCATATCGAG GAAACTGCAA AGACGTGTCC AGGTGTGTGG CCGAAAGGAA 360
GTATAACCCAG GAGCAAGCCC GGAAGGAGTT TCAGCAAGTG TTCATTCCCTG AGTGAATGA 420
CGACGGCACC TACAGTCAGG TCCAGTGCA CAGCTACACG GGATACTGCT GGTGCGTCAC 480
GCCCAACGGG AGGCCCATCA GCGGCACTGC CGTGGCCAC AAGACGCCCC GGTGCCCGGG 540
TTCCGTAAAT GAAAAGTTAC CCCAACGCGA AGGCACAGGA AAAACAGATG ATGCCGCAGC 600
TCCAGCGTTG GAGACTCAGC CTCAAGGAGA TGAAGAAGAT ATTGCATCAC GTTACCCCTAC 660
CCTTTGGACT GAACAGGTTA AAAGTCGGCA GAACAAAACC AATAAGAATT CAGTGTAC 720
CTGTGACCAA GAGCACCAGT CTGCCCTGGA GGAAGCCAAG CAGCCCAAGA ACGACAATGT 780
GGTGATCCCT GAGTGTGCGC ACGGCGGCCT CTACAAGCCA GTGCAGTGCC ACCCCTCCAC 840
GGGGTACTGC TGGTGCCTCC TGGTGGACAC GGGGCGCCCC ATTCCCGGCA CATCCACAAG 900
GTACGAGCAG CCGAAATGTG ACAACACGGG CCAGGGCCCA CCCAGCCAAA GCCCGGGACC 960
TGTACAAGGG CCGCCAGCTA CAAGGTTGTC CGGGTGCCAA AAAGCATGAG TTTCTGACCA 1020
GCGTTCTGGA CGCGCTGTCC ACGGACATGG TCCACGCCGC CTCCGACCCC TCCTCCTCGT 1080
CAGGCAGGCT CTCAGAACCC GACCCCAGCC ATACCCTAGA GGAGCAGGTG GTGCACTGGT 1140
ACTTCAAAC ACTGGATAAA AACTCCAGTG GAGACATCGG CAAAAAGGAA ATCAAACCT 1200
TCAAGAGGTT CCTTCGCAAA AAATCAAAGC CCAAAAAATG TGTGAAGAAG TTTGTTGAAT 1260
ACTGTGACGT GAATAATGAC AAATCCATCT CCGTACAAGA ACTGATGGGC TGCCTGGCG 1320
TGGCGAAAGA GGACGGCAAA GCGGACACCA AGAAACGCCA CACCCCCAGA GGTCAATGCTG 1380
AAAGTACGTC TAATAGACAG CCAAGGAAAC AAGGATAAAAT GGTCATACCC CCGAAGGCAG 1440
TTCCTAGACA CATGGAAAT TTCCCTCACC AAAGAGCAAT TAAGAAAACA AAAACAGAAA 1500
CACATAGTAT TTGCACTTTG TACTTTAAAT GTAAATTACAC TTTGTAGAAA TGAGCTATTT 1560
AAACAGACTG TTTTAATCTG TGAAAATGGA GAGCTGGCTT CAGAAAATTA ATCACATACA 1620
ATGTATGTGT CCTCTTTGA CCTTGGAAAT CTGTATGTGG TGGAGAAGTA TTTGAATGCA 1680
TTTAGGCTTA ATTTCTTCGC CTTCCACATG TTAACAGTAG AGCTCTATGC ACTCCGGCTG 1740
CAATCGTATG GCTTCTCTA ACCCCTGCAG TCACCTCCAG ATGCCTGTGC TTACAGCATT 1800
GTGGAATCAT GTTGGAAAGCT CCACATGTCC ATGGAAGTTT GTGATGTACG GCCGACCCCTA 1860
CAGGCAGTTA ACATGCATGG GCTGGTTGT TTCTTGGAT TTTCTGTTAG TTTGTCTTGT 1920
TTTGCTTCC AGAGATCTTG CTCATACAAT GAATCACGCA ACCACTAAAG CTATCCAGTT 1980
AAGTGCAGGT AGTTCCCTG GAGGAAATAA TATTTCAAA CTGTCGTTGG TGTGATACTT 2040

TGGCTCAAAG GATCTTGCT TTTCCATTAA AAGCTTCTGT TTTGAGTTT GCCCTGGGGC 2100
TTGAATGAGT CCCAGAGAGT CGTCGGATG GTGGGAGGCT GCCTAGGAGG CAGTAAATCC 2160
AGTCACAGTG CCTGGGAGGG GCCCATCCTT CCAAAATGTA AATCCAGTCG CGGTGTGACC 2220
GAGCTGGCTA ACAGGCTTGT CTGCCTGGTT TTCCCTCCTAC ACGTGGACAT TATTCTCCTG 2280
ATCCTCCTAC CTGGTCCACC CCAGGGCTAC CGGAAGGTAA AATCTTCACC TGAACCAATT 2340
ATGAGCAGTC TCCTTACTGA AGGTACAGCC GGATACGTGG TGCCCCCGGG GCTGGTGTG 2400
GCAGCCGGGG GGAGGGCCT GAGGGTCCCC ACGGTTCTT TCTGCTTTTC TGAATGCATC 2460
AAGGGTACGA GAACTTGCCA ATGGGAAATT CATCCGAGTG GCACTGGCAG AGAAGGATAG 2520
GAGTGGAATG CCCACACAGT GACCAACAGA ACTGGTCTGC GTGCATAACC AGCTGCCACC 2580
CTCAGGCCTG GGCCCCAGAG CTCAGGGCAC CCAGTGTCTT AAGGAACCAT TTGGAGGACA 2640
GTCTGAGAGC AGGAACATTCA AGCTGTGATT CTATCTCGC TCAGACTTTT GGTTGGAAAA 2700
AGATCTTCAT GGCCCCAAAT CCCCTGAGAC ATGCCATTGA GAATGATTTC GTGATGTTGT 2760
GATGCTTGTG GAGCATCGCG TAAGGCTTCT TGCTTATTTA AACTGTGCAA GGTAAAAATC 2820
AAGCCTTGG AGCCACAGAA CCAGCTCAAG TACATGCCAA TGTTGTTAA GAAACAGTTA 2880
TGATCCTAAA CTTTTGGAT AATCTTTAT ATTTCTGACC TTTGAATTAA ATCATTGTTTC 2940
TTAGATTAAA ATAAAATATG CTATTGAAAC TAAAAAAA AAAGAGGGGA GAAGAAAAAA 3000
AAAAAGG 3007

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: THYMNOT04
(B) CLONE: 2652271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136 :

CTCTCTGCTC CGGTGCAGGC CCGCAGGCAGC CCTGGGCTGG GAGCAACGCG ACTGACCGTG 60
GTCGTGGGCG GACGGCGGCT GCAGCGTGGA GGAGCTGGGG TCGCTGTGGG TCGCGAACAG 120
AGCCCGGGAC GTGCGCGCTT GGTGCACGAT CCTGAAGGGG AGCTCCGAGG GGCCCGGGTC 180
TCCAGGGCTG CTGCGGCCAT TCCCGGAGCC CGGCGCGGGG CCCGCGAGAT ACTGGTTAG 240
GCCGTCCCAG GGCTCCGGGC GCACCCGGTG GCCGCTGCTG CAGCGGAGGG AGCGCGGGCG 300

PF-0459 US

CGCGGGGGCT CGGAGACAGC GTTTCTCCG GAAGTCTTCC TCGGGCAGCA GGTGGGAAGT 360
GGGAGCCGGA CGGGCAGCTG GCAGCGTTCT CTCCGCAGGT CGGCACCATG CGCCCTGCAG 420
CCCTGCCGG GGCCCTGCTG GGCTGCCTCT GCCTGGCGTT GCTTGCCTG GGCGGTGCGG 480
ACAAGGCCT GCGTGACAAC CATGAGTGGA AAAAACTAAT TATGGTCAG CACTGGCCTG 540
AGACAGTATG CGAGAAAATT CAAAACGACT GTAGAGACCC TCCGGATTAC TGGACAATAC 600
ATGGACTATG GCCCGATAAA AGTGAAGGAT GTAATAGATC GTGGCCCTTC AATTAGAAG 660
AGATTAAGGA TCTTTGCCA GAAATGAGGG CATACTGGCC TGACGTAATT CACTCGTTTC 720
CCAATCGCAG CCGCTTCTGG AAGCATGAGT GGGAAAAGCA TGGGACCTGC GCCGCCAGG 780
TGGATGCGCT CAACTCCCAG AAGAAGTACT TTGGCAGAAG CCTGGAACTC TACAGGGAGC 840
TGGACCTCAA CAGTGTGCTT CTAAAATTGG GGATAAAACC ATCCATCAAT TACTACCAAG 900
TTGCAGATT TAAAGATGCC CTTGCCAGAG TATATGGAGT GATACCCAAA ATCCAGTGCC 960
TTCCACCAAG CCAGGATGAG GAAGTACAGA CAATTGGTCA GATAGAACTG TGCCTCACTA 1020
AGCAAGACCA GCAGCTGCAA AACTGCACCG AGCCGGGGGA GCAGCCGTCC CCCAAGCAGG 1080
AAGTCTGGCT GGCAAATGGG GCCGCCGAGA GCCGGGGTCT GAGAGTCTGT GAAGATGCC 1140
CAGTCTTCTA TCCCCCACCT AAAAAGACCA AGCATTGATG CCCAAGTTT GGAAATATTTC 1200
TGTTTAAAAA AGCATGAGGT AGGCATGTC 1229

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1972 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: LUNGUT11
(B) CLONE: 2746976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137 :

ACAGGGGCTT CCCCTTCGCC GCCGCCGCCG CCGCCGGCCA AGCTCCGCCG CGCCCGCGC 60
CCGCAGGCCGC CATGCAGTTT ATGTTGCTTT TTAGTCGTCA GGGAAAGCTT CGACTGCAAA 120
AATGGTATGT CCCACTATCA GACAAAGAGA AGAGAAAGAT CACAAGAGAA CTTGTTCAGA 180
CCGTTTAGC ACGGAAACCT AAAATGTGCA GCTTCCTGA GTGGCGAGAT CTGAAGATTG 240
TTTACAAAG ATATGCTAGT CTGTATTTT GCTGTGCTAT TGAGGATCAG GACAATGAAC 300
TAATTACCCCT GGAAATAATT CATCGTTATG TGGAATTACT TGACAAGTAT TTCGGCAGTG 360

PF-0459 US

TCTGTGAACT AGATATCATC TTTAATTG AGAAGGCTTA TTTTATTG GATGAGTTTC 420
TTTGAGGAGG GGAAGTCAG GAAACATCCA AGAAAAATGT CCTTAAAGCA ATTGAGCAGG 480
CTGATCTACT GCAGGAGGAT GCGAAAGAAG CTGAAACCCC ACGTAGTGT CTTGAAGAAA 540
TTGGACTGAC ATAACCTCTCC TCCCTTGTG ATGACTTCTT GTGGCATTTC ACACACTGTA 600
GATGGTCACT CCCTCATGT CCATGTTAGC TCATGGTGT AAGATGATGTC TTGTCAGTAT 660
TACTGTTTG CTAAGCCGCT TCATTCATGC CTACACAATT TTTTTTAAA AGGAAACTTT 720
AGTTAATTAA GTGATAAGGG ACTTAAATAT GAATTAGAAT GGTGCAGAAA GAGATACCTT 780
TTCTGGATAT TTTAAAGTTT AAAGGTCAGT TTCTCTTAAT CTGATTATGT GCACATATGA 840
AAATGGCACA TCATATACAT GTAAAATCAG GCAGTATACA TTTATTAATT ACTGTATTG 900
ACAAAGGAAA CTCTAAATT ATAATGTGAA ACCTGGTTT ATGAAACCAA AGACTAGTGC 960
AGCATTTCAG CATATGTAAA AAAAAAAA AAGGGAATTG ACATGTCACA TATCAAATGA 1020
ATGGAAACTT TGTTGAAACT TTAAAAAGCA AATTTACTCC AAAGACTTGT ATTGGAAATT 1080
ACATACCTTT TTTTTTTT TTTAAAGGAC TACAGATTAT TTTTAATGAC TAAATTGGAG 1140
TGATACTTCT TACACTAAAA ATTATTTCTT AGGCATTCTG AATCTGGAT GAGAACAGG 1200
ATTGTTTCAC AATAGTAAGC ACATAATTAA TAAGGCCAAG GCACATTGAC CTCCTGAGAT 1260
GAATTTTG TGGTCATAAT CAAACTTA GTGTTTTG ATGCCCAAA ATAAAGTGAG 1320
AATGGTAATT TGCCAGGAAT TCTTCATAAC AGTATCTTAC AAAAAACGTG TTGCTCTCTT 1380
CACAGTATTA TGTGTAAAGT CATTGTTAA AGCACGAATG TTCCCTCTGG GGTACTTGT 1440
AAAGCTAAAT TTATTTGCT TCCCTCCACT TAGAAGTGCT GCACACTTA CAGCAGCTTC 1500
CTTCTTTCC ATGGCACTGC CTAGTTAACAA GAAGTCTTAT AAAAATTAA AAAGACACAT 1560
TTCTTACAAA AAAGAGTTGA ATGAGGTTAA ATGGCATTAG ATGGCTCTAT ATTTTTTAAA 1620
GCTATGTAAT TGTTCAGCGT CACTTTCTA AGTACTTATA CATATCTAAA CATGTCTCA 1680
TGGTTATAT TTTCACTTAT ATATGCTGGG CTGGATTAAG CTTTGTGTG ATTGTGACCA 1740
ACATTCAAGGC CACGTGAGCA CTGTCTTATC ACATGCCAA TTAGTTGAA TAAACGTTCA 1800
ACGTACAAAC ACTGGAGTGT GTTTTATCT CTTCCAAA GTTTGTCAA CTATGCAGAG 1860
CTGCTGAAGG AAGAATTCT CATTTTTTT TCAGTAAAT GTTGAAAATT CCCCTCCATT 1920
TGAATATGGT GGTTGTTATA AGCACACACA AGATACATGG TGGAAGATCT AG 1972

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1741 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: THP1AZS08
 - (B) CLONE: 2753496

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138 :

CGGGTTCCGG GCTCCGGGCT CTGGGTGGCG GCGGCTGTGA GCNGCGGCTG ANCCNCCGCG 60
CTGCGCANCG ACGCGGAAT GAAGCGGGCG CTGGGCAGGC GAAAGGGCGT GTGGTTGCGC 120
CTGAGGAAGA TACTTTCTG TGTTTGCCCC TTGTACATTG CCATTCCATT TCTCATCAA 180
CTATGTCTG GAATACAGGC CAAACTGATT TTCTTGAATT TCGTAAGAGT TCCCTATTTC 240
ATTGATTGAA AAAAACACAA GGATCAAGGT TTGAATCACA CGTGTAACTA CTACCTGCAG 300
CCAGAGGAAG ACGTGACCAT TGGAGTCTGG CACACCGTCC CTGCAGTCTG GTGGAAGAAC 360
GCCCAAGGCA AAGACCAGAT GTGGTATGAG GATGCCTTGG CTTCCAGCCA CCCTATCATT 420
CTGTACCTGC ATGGGAACGC AGGTACCAAGA GGAGGCGACC ACCGCGTGGA GCTTTACAAG 480
GTGCTGAGTT CCCTTGGTTA CCATGTGGTC ACCTTTGACT ACAGAGGTTG GGGTGACTCA 540
GTGGGAACGC CATCTGAGCG GGGCATGACC TATGACGCAC TCCACGTTT TGACTGGATC 600
AAAGCAAGAA GTGGTGACAA CCCC GTGTAC ATCTGGGCC ACTCTCTGGG CACTGGCGTG 660
GCGACAAATC TGGTGCAGCG CCTCTGTGAG CGAGAGACGC CTCCAGATGC CCTTATATTG 720
GAATCTCCAT TCACTAATAT CCGTGAAGAA GCTAAGAGCC ATCCATTTC AGTGATATAT 780
CGATACTTCC CTGGGTTTGA CTGGTTCTTC CTTGATCCTA TTACAAGTAG TGGAATTAAA 840
TTTGCAAATG ATGAAAACGT GAAGCACATC TCCTGTCCCC TGCTCATCCT GCACGCTGAG 900
GACGACCCGG TGGTGCCTT CCAGCTTGGC AGAAAGCTCT ATAGCATCGC CGCACCAAGCT 960
CGAAGCTTCC GAGATTCAA AGTCAGTT GTGCCCTTTC ATTCAGACCT TGGCTACAGG 1020
CACAAATACA TTTACAAGAG CCCTGAGCTG CCACGGATAC TGAGGGAATT CCTGGGGAAAG 1080
TCGGAGCCTG AGCACCAGCA CTGAGCCTGG CCGTGGGAAG GAAGCATGAA GACCTCTGCC 1140
CTCCTCCCGT TTTCTTCCAG TCAGCAGCCC GGTATCCTGA AGCCCCGGGG GGCGGGCACC 1200
TGCAATGCTC AGGAGCCCAG CTCGCACCTG GAGAGCACCT CAGATCCCAG GTGGGGAGGC 1260
CCCTGCAGGC CTGCAGTGCC CGGAGGCCTG AGCATGGCTG TGTGGAAAGC GTGGGTGGCA 1320
GGCATGTGGC TCTCCTTGCC GCCCCTCAAC CTGAGATCTT GTTGGGAGAC TTAATGGCAG 1380
CAGGCAGCCA TCACTGCCTG GTTGATGCTG CACTGAGCTG GACAGGGGA GTCCGGGCAG 1440
GGGACTCTTG GGGCTCGGGGA CCATGCTGAG CTTTTGGCA CCACCCACAG AGAACGTGGG 1500

GTCCAGGTTTC TTTCTGCACC TTCCCAGCAC ATGCAGAATG ACTCCAGTGG TTCCATCGTC 1560
CCCTCCTGCC CTGTGTACCT GCTTGCCTTT CTCAGCTGCC CCACCTCCCC TGGGCTGGCC 1620
CACTCACCCA CAGTGGAACT GCCCGGGATC TGCACTTCCCT CCCCTTTCAC CTACCTGTAC 1680
ACCTAACCTG GCCTTAGACT GAGCTTTATT TAAGAATAAA ATCGTGGTGG TGAAAAAAA 1740
A 1741

(2) INFORMATION FOR SEQ ID NO: 139:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2808 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: OVARTUT03
(B) CLONE: 2781553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139 :

GGCAAGATGG CGGAAGGGGA GGACGTGGGA TGGTGGCGGA GCTGGCTGCA GCAGAGCTAC 60
CAAGCAGTCA AAGAGAAGTC CTCTGAAGCC TTGGAGTTA TGAAGCAGGGAA CCTGACGGAG 120
TTTACCCAGG TGGTGCAGCA TGACACGGCC TGTACCATCG CAGCCACGGC CAGCGTGGTC 180
AAGGAGAAGC TGGCTACGGA AGGCTCCTCA GGAGCAACAG AGAAGATGAA GAAAGGGTTA 240
TCTGACTTCC TAGGGGTGAT CTCAGACACC TTTGCCCTT CGCCAGACAA AACCATCGAC 300
TGCATGTCA TCACCCCTGAT GGGCACACCG TCTGGCACAG CTGAGCCCTA TGATGGCACC 360
AAGGCTCGCC TCTATAGCCT GCAGTCGGAC CCAGCAACCT ACTGTAATGA ACCAGATGGG 420
CCCCCGGAAT TGTTGACGC CTGGCTTCC CAGTTCTGCT TGGAGGAGAA GAAGGGGGAG 480
ATCTCAGAGC TCCTTGTAGG CAGCCCCCTCC ATCCGGGCC TCTACACCAA GATGGTTCCA 540
GCAGCTGTT CCCATTCAAG ATTCTGGCAT CGGTATTCT ATAAAGTCCA TCAGTTAGAG 600
CAGGAGCAGG CCCGGAGGGGA CGCCCTGAAG CAGCGGGCGG AACAGAGCAT CTCTGAAGAG 660
CCCGGCTGGG AGGAGGAGGA AGAGGAGCTC ATGGGCATT CACCCATATC TCCAAAAGAG 720
GCAAAGGTTTC CTGTGGCCAA AATTCTACA TTCCCTGAAG GAGAACCTGG CCCCCAGAGC 780
CCCTGTGAAG AGAATCTGGT GACTTCAGTT GAGCCCCAG CAGAGGTGAC TCCATCAGAG 840
AGCAGTGAGA GCATCTCCCT CGTGACACAG ATCGCCAACC CGGCCACTGC ACCTGAGGCA 900
CGAGTGCTAC CCAAGGACCT GTCCCAAAAG CTGCTAGAGG CATCCTTGGA GGAACAGGGC 960
CTGGCTGTGG ATGTGGGTGA GACTGGACCC TCACCCCTA TTCACTCCAA GCCCCTAACG 1020

CCTGCTGGCC ACACCGGCAG CCCAGAGCCC AGGCCTCCAG CCAGAGTAGA GACTCTGAGG 1080
GAGGAGGCGC CCACAGACTT ACGGGTGTT GAGCTGAAC CGGATAGTGG GAAGTCTACA 1140
CCCTCCAACA ATGGAAAGAA AGGCTCAAGC ACGGACATCA GTGAGGACTG GGAGAAAGAC 1200
TTTGACTTGG ACATGACTGA AGAGGAGGTG CAGATGGCAC TTTCCAAAGT GGATGCCTCC 1260
GGGGAGCTGG AAGATGTAGA GTGGGAGGAC TGGGAGTGAG GGAGCCAGAG GGAGCAGCTC 1320
CCCCACCCAT GGCATCTCTC GCCTCCCTCG CTCGTCTCAG CCCAGCCCTG GAAGACTGAG 1380
AATGTTCCCC CAAATCTCCT CTGCCAACCA GAGCTCTGGG CACAGATTCT GGTGGCTCCC 1440
TGCTGGCCCT CTTGGGCCTC TGCTCACACC TGGGAAGGGG CTCTCTAAAT CCCGGCCAGA 1500
AACTCTGACT TGTGCCAACCA ATAGGATGAC CCAAGGGAGA GGAAACCTAT CCTCCTCACC 1560
AGAAGAGCCT GTGTTTTCT GCTGAACACC CACTGTTCT GAGGACTCCT GCTGGGAAGT 1620
CCCAAGGGAT AGTTCTAGCC CTTCTGCCTG TGTAGACAGA AGCTAAACCA CCAGTCTCTC 1680
TCGGAGGAAG CTGAGACAAC ATACTCTGTC CATACTATAAG CAGGCAGGGA GGGCCATGCC 1740
ACCTACCCTT GGCTAAACAG GGACAGTGAA CACATTTGG TTCCTATCCC AGTGGGTAAG 1800
AGGCACTTAT CTCTGGAAA TTTGCCTCTC TTGGGACTCT CCCCTCCCCA GGCATTTCC 1860
ATTCCTGGAA AGGCTCCTT GGGGTTTCAGA ATCCAGAGAC CAAACCTGA CCCACCTCCT 1920
TCCTTTCTC CAGCCCACGC TGGTCTGTCC CCATGCCTTC CCAGGGCTTC TTCATGTCA 1980
ATGCACCCAA GTCCTTAGCC CAGCTGTGCC ACCTGCAGGA GTTCGCTCTT GCGTTCTTC 2040
CCCTCCCCAA GAAGGGAGGG GGCTACTTCA GGCCCTTCTG TGTGTTGCCT GGCAGGATAC 2100
CTTGTCCAAC CAGCTACCCA CCTCAACTCC CCTGTAGTTT AGGACACAAA ACAGCTACCA 2160
GCGGTACAGA GCGGTGATCA AAGCCGAGTA CTTACAACCTC TGGTAAGCCT AGCTTCTCCG 2220
CCTCAGCCCT TCTGCTTCTG GAAGGGCTAT CCTGGGGGTG AACTTGAAAC TCTCATCAGG 2280
CTTCTGAAA AGCTCTCTT CCTGAAGACA GACCCAGCCT TTGTGCTCTC ACCCTCCACT 2340
CTGGTAAAGC TGCACCTCTG GGGGAATGAG GGGCTGCAGG AATCTCTGGA GAGCCTGGTG 2400
CTTCACGATG CTGCTCTGGT GATTCTTGT A CCTAATCTGG TGTGCTCACC AATGAGTGAA 2460
AGGGATCGTG GGTCAGGGAC ACCGAGAGAG TGAGGTCACT TCCACTTCAA ACCTTCAGTG 2520
AGGGGGTGGG ATGGAGAGAA TGCTGAATCT TTTTTTGAC GGGATGGGGT TTTTCTCTT 2580
GTAATTATTT CTTTAGTTA ATTAACCTTT TGGTTGTTG TGCAATATTA TATATTTAA 2640
ATTATAATGC ATCTCCCCAG AGTATTTGT AGCTGGAAA AGAAAAAAGG AAAAAAAGAA 2700
AAAAAGATTG TAACAGCTGT TAGTTTATA ATTAAAAAAG AAAGAAAAAA GAACTTTGTC 2760
CTGAACCTTT TACAGACTTG CCGTTAACAG CATTAAAGTG ATTCAACCC 2808

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 717 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: ADRETUT06
(B) CLONE: 2821925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140 :

CATGCGCCGA CCTTCCTCGG CTGGATTAC ANGTTNNCCC TTAACACCCG GGATTAAAGG 60
GACCCACACT ACCTTCCCGA AGTTGAAGGC AAGCGGTGAT TGTGTTGAGA CGGCGCTTG 120
TCATGGGACC TGTGCGGTTG GGAATATTGC TTTTCCTTTT TTTGGCCGTG CACGAGGCTT 180
GGGCTGGGAT GTTGAAGGAG GAGGACGATG ACACAGAACG CTTGCCAGC AAATGCGAAG 240
TGTGTAAGCT GCTGAGCACA GAGCTACAGG CGGAACTGAG TCGCACCGGT CGATCTCGAG 300
AGGTGCTGGA GCTGGGGCAG GTGCTGGATA CAGGCAAGAG GAAGAGACAC GTGCCTTACA 360
GCGTTTCAGA GACAAGGCTG GAAGAGGCCT TAGAGAATTG ATGTGAGCGG ATCCTGGACT 420
ATAGTGTCA CGCTGAGCGC AAGGGCTCAC TGAGATATGC CAAGGGTCAG AGTCAGACCA 480
TGGCAACACT GAAAGGCCTA GTGCAGAAGG GGGTGAAGGT GGATCTGGGG ATCCCTCTGG 540
AGCTTTGGG ATGAGCCCAG CCGTTGAGGT CACATACCTC AAGAAGCAGT GTGAGACCAT 600
GTTNGAGGAG TTTGAGACA TTGTGGGAGA CTGGTACTTG CACCATCAGG AGCAGCCGCT 660
ACAAGATTG CTCTGTGAAG GTCATGTGCT GCCAGCTGCT TGAACACTGCAT GTCGGGT 717.

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2552 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: UTRSTUT05
(B) CLONE: 2879068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141 :

GGCAGGGGGC GCGCCGGGCC CAGCGCCACG TCACCGCCCA GCAGCCCTCC CGATTGGCGG 60
CGGGGGCGGC TATAAAGGGA GGGCGCAGGC GGCAGCCCGGA TCTCTCCGC CGCCATTAA 120

AATCCAGCTC CATACAACGC TCCGCCGCCG CTGCTGCCGC GACCCGGACT GCGGCCAGC 180
ACCCCCCTGC CGACAGCTCC GTCACTATGG AGGATATGAA CGAGTACAGC AATATAGAGG 240
AATTGCAGA GGGATCCAAG ATCAACCGCA GCAAGAATCA GCAGGATGAC GGTAAAATGT 300
TTATTGGAGG CTTGAGCTGG GATACAAGCA AAAAAGATCT GACAGAGTAC TTGTCTCGAT 360
TTGGGGAAAGT TGTAGACTGC ACAATTAAA CAGATCCAGT CACTGGGAGA TCAAGAGGAT 420
TTGGATTGT GCTTTCAAA GATGCTGCTA GTGTTGATAA GGTTTGGAA CTGAAAGAAC 480
ACAAACTGGA TGGCAAATTG ATAGATCCCA AAAGGGCAA AGCTTAAAA GGGAAAGAAC 540
CTCCCAAAAA GGTTTTGTG GGTGGATTGA GCCCGGATAC TTCTGAAGAA CAAATTAAAG 600
AATATTTGG AGCCTTGGA GAGATTGAAA ATATTGAAC TCCCATGGAT ACAAAAACAA 660
ATGAAAGAAC AGGATTGTG TTTATCACAT ATACTGATGA AGAGCCAGTA AAAAATTGT 720
TAGAAAGCAG ATACCATCAA ATTGGTTCTG GGAAGTGTGA AATCAAAGTT GCACAACCCA 780
AAGAGGTATA TAGGCAGCAA CAGCAACAAAC AAAAAGGTGG AAGAGGTGCT GCAGCTGGTG 840
GACGAGGTGG TACGAGGGGT CGTGGCCGAG GTCAGGGCCA AACTGGAAC CAAGGATTAA 900
ATAACTATTA TGATCAAGGA TATGGAAATT ACAATAGTGC CTATGGTGGT GATCAAAACT 960
ATAGTGGCTA TGGCGGATAT GATTATACTG GGTATAACTA TGGGAACAT GGATATGGAC 1020
AGGGATATGC AGACTACAGT GGCAACAGA GCACTTATGG CAAGGCATCT CGAGGGGGTG 1080
GCAATCACCA AAACAATTAC CAGCCATACT AAAGGAGAAC ATTGGAGAAA ACAGGTGTGT 1140
ATAAGAGTAC AGGAAAACAG TAGAAATGTC TAATTAAATT TAAAGATCAA TAGACAAATG 1200
AAACGTAAAA ACAAAATACT ATGTAGCCTG TTTTACTAA ATTGTTGATT TTTAATTGC 1260
TTTATGAGCC TGTTTGCCT AAAGTGTCTA TAGATCTTA ACTTTAAAGT CTTATCTCAC 1320
TTCTTTAGT ATTGCAGAAA AACTTAAGAG TTTTCTGTT TGCTTTGTG TACCAGGTGG 1380
TCTAGAGGAA TAATTAAACA TTTTAGAACT ATTAACAGGT AAAGTACTGA AATGGGTACA 1440
ACTTAAGGAA AACAAAGAATG TTGTCTCTA ACTCTGACAT TATACCTTGT TTGTACCCGC 1500
CAGCGGGAAC TTCATTGCAG GCCGTGTGTC ACCCTGACCA CGTCTATCTC TGGGGGTGCG 1560
ACGTTGCAGG CAGAGCGCAA GGCATACACC AGAAAACGCT GTCCTGTGGT ATGGTCTCTT 1620
CCAACCTCAT GTACCAGCGT AAAGATTAAG GTGGAAAAGT TCAGACTTTG GCTTCATTAA 1680
TAATCTTTT GGAGATTAAG TGTCTAAACT TAACTTAAAT GGTTTTTAC AGGAGTTAAA 1740
GTACATAAT GCCTTTTAC AGCTTAATCA TTTGGTCTT CTGTTAGTG TTGTATTCA 1800
ATTGTGGAGC CTCATTTAA GTGTTCATTC TTTAAGATT TAATGCTTGC TTTTCTTTT 1860
TATAGCTAAT AGTGAATCT ACAAAACAAA ACAAGAACTT TTAAATCTGG GATATAAATT 1920
AAAGATCATA TGCACAGATC AATTTATGTT CTTGTAATAA ACTTATTAGA AATTGGTGT 1980

TGTGATAGCA TTTTACTTGG GTTACTAGAG ATGCTTCTAG TAGACCTTAA TCTAGCATAG 2040
TTGAACCTCT GAATATGGGA AGGTTGTATT CCCAGATTCT TTCCTGAATA GATTTGAATT 2100
TAATGTCATT TGGGAACTCC AGGGTGAGTT TATTGACTAC CCAAACGTAA TTTTACCAAT 2160
AAATATGCAT ATGATCTTTA ATTATTGAAG AAAATAAAGT GAGGACTTAA AACAAATTCA 2220
GAAAGTGGAC CTTTAAAAGC TTGTCAGAGT TGACACAAATC TAACTGGTAT TTTGTTTTG 2280
TTTTTAGGAG GAGATGTTAA AGTAACCCAT CTTGCAGGAC GACATTGAAG ATTGGTCTTC 2340
TGTTGATCTA AGATGATTAT TTTGTAAG ACTTTCTAGT GTACAAGACA CCATTGTGTC 2400
CAACTGTATA TAGCTGCCAA TTAGTTTCT TTGTTTTAC TTTGTCCTTT GCTATCTGTG 2460
TTATGACTCA ATGTGGATTT GTTTATACAC ATTTTATTG TATCATTCA TGTTAAACCT 2520
CAAATAAATG CTTCCTTATG TGAAAAAAA AA 2552

(2) INFORMATION FOR SEQ ID NO: 142:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1046 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: SINJNOT02
(B) CLONE: 2886757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142 :

TACCACTGTA AAGCCAGAGC TGAGGTTCTT GATAGTCCAC AATGGGTGAA CCACAGCAAG 60
TGAGTGCACT TCCACCACCT CCAATGCAAT ATATCAAGGA ATATACGGAT GAAAATATT 120
AAGAAGGCTT AGCTCCCAAG CCTCCCCCTC CAATAAAAGA CAGTTACATG ATGTTGGCA 180
ATCAGTTCCA ATGTGATGAT CTTATCATCC GCCCTTGGA AAGTCAGGGC ATCGAACGGC 240
TTCATCCTAT GCAGTTGAT CACAAGAAAG AACTGAGAAA ACTTAATATG TCTATCCTTA 300
TTAATTCTT GGACCTTTA GATATTTAA TAAGGAGCCC TGGGAGTATA AAACGAGAAG 360
AGAAAATAGA AGATCTTAAG CTGCTTTTG TACACGTGCA TCATCTTATA AATGAATACC 420
GACCCCACCA AGCAAGAGAG ACCTTGAGAG TCATGATGGA GGTCCAGAAA CGTCAACGGC 480
TTGAAACAGC TGAGAGATTT CAAAAGCACC TGGAACGAGT AATTGAAATG ATTCAGAATT 540
GCTTGGCTTC TTTGCCTGAT GATTTGCCTC ATTCAAGAAGC AGGAATGAGA GTAAAAACTG 600
AACCAATGGA TGCTGATGAT AGCAACAATT GTACTGGACA GAATGAACAT CAAAGAGAAA 660
ATTCAGGTCA TAGGAGAGAT CAGATTATAG AGAAAGATGC TGCCTTGTGT GTCCTAATTG 720

ATGAGATGAA TGAAAGACCA TGAAAGATGT TTCTTTCTT TTTTTCCCTT TTGATAATAG 780
 CATCATATAT TAGTCATTT TCTTTGGAC AGTCTTAAGA GAAGTTCAC TAAAAATGTA 840
 AACAGCTTTA ATCTTGACTC CAAATTTTC AATTATGAGA TGTCTAGGC AGTAATTCG 900
 CTGTATAACA AGCATAGACA AATGAGTGTC CCTGCACTAA GAAGAATCAC TTTAAAAAGC 960
 AAAGTGTAG CTGCTGTTGT ATGGGACATT CCTATGTTT AGAGTTGCAG TAAAACTTG 1020
 ATGATAACCT CAAAAAAA TAAAAA 1046

(2) INFORMATION FOR SEQ ID NO: 143:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1864 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: SCORN0T04
 - (B) CLONE: 2964329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143 :

GCCCTGGGCT CGCGGCGGTG CCGCGGGGAT GGCGGGAGCC GGAGCTGGAG CCGGAGCTCG 60
 CGGCGGAGCG CGGGCGGGGG TCGAGGCTCG AGCTCGCGAT CCACCGCCCG CGCACCGCGC 120
 ACATCCTCGC CACCCCTCGGC CTGCGGCTCA GCCCTCGGCC CGCAGGATGG ATGGCGGGTC 180
 AGGGGGCCTG GGGTCTGGGG ACAACGCCCG GACCACTGAG GCTCTTTCG TGGCACTGGG 240
 CGCGGGCGTG ACGGCGCTCA GCCATCCCC GCTCTACGTG AAGCTGCTCA TCCAGGTGGG 300
 TCATGAGCCG ATGCCCCCCA CCCTTGGGAC CAATGTGCTG GGGAGGAAGG TCCTCTATCT 360
 GCCGAGCTTC TTCACCTACG CCAAGTACAT CGTGCAAGTG GATGGTAAGA TAGGGCTGTT 420
 CCGAGGCCTG AGTCCCCGGC TGATGTCCAA CGCCCTCTCT ACTGTGACTC GGGTAGCAT 480
 GAAGAAGGTT TTCCCTCCAG ATGAGATTGA GCAGGTTTCC AACAAAGGATG ATATGAAGAC 540
 TTCCCTGAAG AAAGTTGTGA AGGAGACCTC CTACGAGATG ATGATGCAGT GTGTGTCCCG 600
 CATGTTGGCC CACCCCCCTGC ATGTCATCTC AATGCGCTGC ATGGTCCAGT TTGTGGGACG 660
 GGAGGCCAAG TACAGTGGTG TGCTGAGCTC CATTGGGAAG ATTTCAAAG AGGAAGGGCT 720
 GCTGGGATTG TTCGTTGGAT TAATCCCTCA CCTCCTGGGC GATGTGGTTT TCTTGTGGGG 780
 CTGTAACCTG CTGGCCCACT TCATCAATGC CTACCTGGTG GATGACAGCT TCAGCCAGGC 840
 CCTGGCCATC CGGAGCTATA CCAAGTCGT GATGGGGATT GCAGTGAGCA TGCTGACCTA 900
 CCCCTTCCTG CTAGTTGGCG ACCTCATGGC TGTGAACAAC TGCGGGCTGC AAGCTGGGCT 960

PF-0459 US

CCCCCCTTAC TCCCCAGTGT TCAAATCCTG GATTCACTGC TGGAAGTACC TGAGTGTGCA 1020
GGGCCAGCTC TTCCGAGGCT CCAGCCTGCT TTTCCGCCGG GTGTCATCAG GATCGTGCTT 1080
TGCCCTGGAG TAACCTGAAT CATCTAAAAA ACACGGTCTC AACCTGGCCA CCGTGGGTGA 1140
GGCCTGACCA CCTTGGGACA CCTGCGAGAC GACTCCAACC CAACAACAAC CAGATGTGCT 1200
CCAGCCCAGC CGGGCTTCAG TTCCATATTT GCCATGTGTC TGTCCAGATG TGGGGTTGAG 1260
CGGGGGTGGG GCTGCACCCA GTGGATTGGG TCACCCGGCA GACCTAGGGA AGGTGAGGCG 1320
AGGTGGGGAG TTGGCAGAAT CCCCATACCT CGCAGATTTG CTGAGTCTGT CTTGTGCAGA 1380
GGGCCAGAGA ATGGCTTATG GGGGCCAGG TTGGATGGGG AAAGGCTAAT GGGTCAGAC 1440
CCCACCCCGT CTACCCCTCC AGTCAGCCCA GCGCCCATCC TGCAGCTCAG CTGGGAGCAT 1500
CATTCTCCTG CTTTGTACAT AGGGTGTGGT CCCCTGGCAC GTGCCACCA TCATGTCTAG 1560
GCCTATGCTA GGAGGCAAAT GGCCAGGCTC TGCCTGTGTT TTTCTCAACA CTACTTTCT 1620
GATATGAGGG CAGCACCTGC CTCTGAATGG GAAATCATGC AACTACTCAG AATGTGTCT 1680
CCTCATCTAA TGCTCATCTG TTTAATGGTG ATGCCTCGCG TACAGGATCT GGTTACCTGT 1740
GCAGTTGTGA ATACCCAGAG GTTGGGCAGA TCAGTGTCTC TAGTCCTACC CAGTTTAAA 1800
GTTCATGGTA AGATTGACC TCATCTCCCG CAAATAATG TATTGGTGAT TTGGAAAAAA 1860
AAAA 1864

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2295 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: SCORN0T04
(B) CLONE: 2965248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144 :

GTCTGCAGCT CCGGCCGCCA CTTGCGCCTC TCCAGCCTCC GCAGGCCAA CCGCCGCCAG 60
CACCATGGCC AGCACCATTT CCGCCTACAA GGAGAAGATG AAGGAGCTGT CGGTGCTGTC 120
GCTCATCTGC TCCTGCTTCT ACACACAGCC GCACCCCAAT ACCGTCTACC AGTACGGGGA 180
CATGGAGGTG AAGCAGCTGG ACAAGCGGGC CTCAGGCCAG AGCTTCGAGG TCATCCTCAA 240
GTCCCCTTCT GACCTGTCCC CAGAGAGCCC TATGCTCTCC TCCCCACCCA AGAAGAAGGA 300
CACCTCCCTG GAGGAGCTGC AAAAGCGGCT GGAGGCAGCC GAGGAGCGGA GGAAGACGCA 360

GGAGGGCGCAG GTGCTGAAGC AGCTGGCGGA CGGCGCGAGC ACGAGCGCGA GGTGCTGCAC 420
 AAGGCGCTGG AGGAGAATAA CAACTTCAGC CGCCAGGCAG AGGAGAAGCT CAACTACAAG 480
 ATGGAGCTCA GCAAGGGAGAT CCGCGAGGCA CACCTGGCCG CACTGCAGCA GCGGCTGCAC 540
 GAGAAGGAGC TGCACGCGGC CGAGGTGCAG AGGAACAAAGG AGCAGCGAGA AGAGATGTCG 600
 GGCTAAGGGC CGGGGACGGG CGGCGCCCAT CCTGCAGCG AACACGTTCG GTTTTGGTT 660
 TTGTTTCGTT CACCTCTGTC TAGATGCAAC TTTGTTCCCT CCTCCCCCAC CCCAGCCCC 720
 AGCTTCATGC TTCTCTTCCG CACTCAGCCG CCCTGCCCTG TCCTCGTGGT GAGTCGCTGA 780
 CCACGGCTTC CCCTGCAGGA GCCGCCGGGC GTGAGACGCG GTCCCTCGGT GCAGACACCA 840
 GGCCGGGCGC GGCTGGGTCC CCCGGGGGCC CTGTGAGAGA GGTGGTGGTG ACCGTGGTAA 900
 ACCCAGGGCG GTGGCGTGGG ATCGCGGGTC CTTACGCTGG GCTGTCTGGT CAGCACGTGC 960
 AGGTCAAGGGC AGGTCCCTCTG AGCCGGCGCC CCTGGCCAGC AGGCGAGGCT ACAGTACCTG 1020
 CTGTCTTCC AGGGGAAAGG GGCTCCCCAT GAGGGAGGGG CGACGGGGGA GGGGGGTGAT 1080
 GGTGCCTGGG AGCCTGCGTG TGCAGCCGGT GCTTGTGAA CTGGCAGGCG GGTGGGTGGG 1140
 GGCTGCAGCT TTCCCTTAATG TGGTTGCACA GGGGTCTCT GAGACCACCT GGCGTGAGGT 1200
 GGACACCCTG GCCCTTCCTG GAAGCCTGCA GTTGGGGGCC TGCCCTGAGT CTGCTGGGA 1260
 GTGGGCATTC TCTGCCAGGG ACCCATGAGC AGGCTGCATG GTCTAGAGGT TGTGGCAGC 1320
 ATGGACAGTC CCCCACTCAG AAGTGCAAGA GTTCCAAAGA GCCTCTGGCC CAGGCCCTC 1380
 CGTGGGACAG CCCCCCGGCC CCTCCCCACC AGGGCTTGC AGATGTCCTT GAAAGACCCA 1440
 CCCTAGAGCC CTTTGGAGTG CTGGCCCCTC CTGTGCCCTC TGCCCTGGTG GAAGCGGCAG 1500
 CCACAAGTCC TCCTCAGGGA GCCCCAAGGG GGATTTGTG GGACCGCTGC CCACAGATCC 1560
 AGGTGTTGGA AGGGCAGCGG GTAAGGTTCC CAAGCCAGCC CCAACACCCCT TCCCACTTGG 1620
 CACCCAGAGG GGGCTGTGGG TGGAGGCCTG ACTCCAGGCC TCTCCCTGCC ACACCCCTCTG 1680
 GGCTGAGTTC CTTCTTCCC TTGGACGCC AGTGCTGGCC TTGGAGGACG GTCAGCTGGA 1740
 GGATGGCGGT GGGGGAGGCT GTCTTGTAC CACTGCAGCA TCCCCACTT CTCCACGGAA 1800
 GCCCCATCCC AAAGCTGCTG CCTGGCCCCCT TGCTGTAAAG TGTGAAGGGG GCGGCTGAGT 1860
 TCTCTTAGGA CCCAGAGCCA GGGCCCTCAA CTTCCATCCT GCGGGAGGCC TTGGCCGGGC 1920
 ACTGCCAGTG TCTTCCAGAG CCACACCCAG GGACCACGGG AGGATCCTGA CCCCTGCAGG 1980
 GCTCAGGGGT CAGCAGGGAC CCACTGCCCT ATCTCCCTCT CCCCACCAAG ACAGCCCCAG 2040
 AAGGAGCAGC CAGCTGGAT GGGAAACCAA GGCTGTCCAC ATCTGGCTTT TGTGGGACTC 2100
 AGAAAGGGAA GCAGAACTGA GGGCTGGAT ATTCCCTCATG GTGGCAGCGC TCATAGCGAA 2160
 AGCCTACTGT AATATGCACC CATCTCATCC ACGTAGTAAA GTGAACCTAA AAATTCAATC 2220

AAATGAACAA TTAAATAAAC ACCTGTGTGT TTAAGACAAA ATAAAAATGG AGGAGAACAA 2280
 AAAAAAAAGGG GCGGT 2295

(2) INFORMATION FOR SEQ ID NO: 145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 842 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: TLYMNOT06
 - (B) CLONE: 3000534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145 :

CGGGGACGGA AGCAGCCCCT GGGCCCGAGG GGCTCGAGGC CGGGCCGGGG CGATGTGGAG 60
 CGCGGGCCGC GGCGGGGCTG CCTGGCCGGT GCTGTTGGGG CTGCTGCTGG CGCTGTTAGT 120
 GCCGGGCGGT GGTGCCGCCA AGACCGGTGC GGAGCTCGTG ACCTGCGGGT CGGTGCTGAA 180
 GCTGCTCAAT ACGCACCAACC GCGTGCGGCT GCACCTCGCAC GACATCAAAT ACGGATCCGG 240
 CAGCGGCCAG CAATCGGTGA CCGGCGTAGA GGCGTCGGAC GACGCCAATA GCTACTGGCG 300
 GATCCGCGGC GGCTCGGAGG GCGGGTGCC GCGCGGGTCC CCGGTGCGCT GCGGGCAGGC 360
 GGTGAGGCTC ACGCATGTGC TTACGGGCAA GAACCTGCAC ACGCACCACT TCCCCTCGCC 420
 GCTGTCCAAC AACCAAGGAGG TGAGTGCCTT TGGGGAAGAC GGCGAGGGCG ACGACCTGGA 480
 CCTATGGACA GTGCGCTGCT CTGGACAGCA CTGGGAGCGT GAGGCTGCTG TGCGCTTCCA 540
 GCATGTGGGC ACCTCTGTGT TCCTGTCAGT CACGGGTGAG CAGTATGGAA GCCCCATCCG 600
 TGGCAGCAT GAGGTCCACG GCATGCCAG TGCCAACACG CACAATACGT GGAAGGCCAT 660
 GGAAGGCATC TTCATCAAGC CTAGTGTGGA GCCCTCTGCA GGTACGATG AACTCTGAGT 720
 GTGTGGATGG ATGGGTGGAT GGAGGGTGGC AGGTGGGGCG TCTGCAGGGC CACTCTTGGC 780
 AGAGACTTTG GGTTGTAGG GGTCCTCAAG TGCCTTGTTG ATTAAAGAAT GTTGGTCTAA 840
 AA 842

(2) INFORMATION FOR SEQ ID NO: 146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2345 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: HEAANOT01
(B) CLONE: 3046870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146 :

GTCCCCGCCCC GCAGCTGCGC GCAGGCGCTC GACGAGCCGC TCGCATTCTA CGTAACGGAC 60
GGCGGAGGCT ACGTGAAGAG AGGCGCGGCG TGACTGAGCT ACGGTTCTGG CTGCGTCCTA 120
GAGGCATCCG GGGCAGTAAA ACCGCTGCGA TCGCGGAGGC GGCGGCCAGG CCGAGAGGCA 180
GGCCGGGCAG GGGTGTGCGA CGCAGGGCGC TGGGCCGGGT TTCGGCTTCG GCCACAGCTT 240
TTTTCTCAA GGTGCAATGA AAGCCTTCCA CACTTTCTGT GTTGTCTTC TGGTGTGG 300
GAGTGTCTCT GAAGCCAAGT TTGATGATTT TGAGGATGAG GAGGACATAG TAGAGTATGA 360
TGATAATGAC TTGCGCTGAAT TTGAGGATGT CATGGAAGAC TCTGTTACTG AATCTCCTCA 420
ACGGGTCATA ATCACTGAAG ATGATGAAGA TGAGACCACT GTGGAGTTGG AAGGGCAGGA 480
TGAAAACCAA GAAGGAGATT TTGAAGATGC AGATACCCAG GAGGGAGATA CTGAGAGTGA 540
ACCATATGAT GATGAAGAAT TTGAAGGTTA TGAAGACAAA CCAGATACTT CTTCTAGCAA 600
AAATAAAGAC CCAATAACGA TTGTTGATGT TCCTGCACAC CTCCAGAAC GCTGGGAGAG 660
TTATTATCTA GAAATTTGA TGGTGACTGG TCTGCTTGCT TATATCATGA ATTACATCAT 720
TGGGAAGAAT AAAAACAGTC GCCTTGACACA GGCTGGTTT AACACTCATA GGGAGCTTT 780
GGAGAGCAAC TTTACTTTAG TGGGGGATGA TGGAACTAAC AAAGAAGCCA CAAGCACAGG 840
AAAGTTGAAC CAGGAGAATG AGCACATCTA TAACCTGTGG TGTTCTGGTC GAGTGTGCTG 900
TGAGGGCATG CTTATCCAGC TGAGGTTCC CAAGAGACAA GACTTACTGA ATGTCCTGGC 960
CCGGATGATG AGGCCAGTGA GTGATCAAGT GCAAATAAAA GTAACCAGTGA ATGATGAAGA 1020
CATGGATACC TACGTATTTG CTGTTGGCAC ACGGAAAGCC TTGGTGCGAC TACAGAAAGA 1080
GATGCAGGAT TTGAGTGAGT TTTGTAGTGA TAAACCTAAC TCTGGAGCAA AGTATGGACT 1140
GCCGGACTCT TTGGCCATCC TGTCAGAGAT GGGAGAAGTC ACAGACGGAA TGATGGATAC 1200
AAAGATGGTT CACTTCTTA CACACTATGC TGACAAGATT GAATCTGTTC ATTTTCAGA 1260
CCAGTTCTCT GGTCCAAAAA TTATGCAAGA GGAAGGTCAG CCTTTAAAGC TACCTGACAC 1320
TAAGAGGACA CTGTTGTTA CATTAAATGT GCCTGGCTCA GGTAACACTT ACCCAAAGGA 1380
TATGGAGGCA CTGCTACCCC TGATGAACAT GGTGATTTAT TCTATTGATA AAGCCAAAAA 1440
GTTCCGACTC AACAGAGAAG GCAAACAAAA AGCAGATAAG AACCGTGCCC GAGTAGAAGA 1500
GAACTTCTTG AAACTGACAC ATGTGCAAAG ACAGGAAGCA GCACAGTCTC GGCGGGAGGA 1560

PF-0459 US

GAAAAAAAGA GCAGAGAAGG AGCGAACAT GAATGAGGAA GATCCTGAGA AACAGCGCAG 1620
GCTGGAGGAG GCTGCATTGA GGCAGTGAGCA AAAGAAGTTG GAAAAGAAGC AAATGAAAAT 1680
GAAACAAATC AAAGTGAAG CCATGTAAAG CCATCCCAGA GATTTGAGTT CTGATGCCAC 1740
CTGTAAGCTC TGAATTACACA GGAAACATGA AAAACGCCAG TCCATTCTC AACCTTAAAT 1800
TTCAGACAGT CTTGGGCAAC TGAGAAATCC TTATTCATC ATCTACTCTG TTTGGGGTT 1860
GGGGTTTTAC AGAGATTGAA GATACCTGGA AAGGGCTCTG TTTCAAGAAT TTTTTTTCC 1920
AGATAATCAA ATTATTTGA TTATTTATA AAAGGAATGA TCTATGAAAT CTGTGTAGGT 1980
TTTAAATATT TTAAAAATTAA TAATACAAAT CATCAGTGCT TTTAGTACTT CAGTGTAA 2040
AGAAATACCA TGAAATTTAT AGGTAGATAA CCAGATTGTT GCTTTTGTT TAAACCAAGC 2100
AGTTGAAATG GCTATAAAGA CTGACTCTAA ACCAAGATTG TGCAAATAAT GATTGGAATT 2160
GCACAATAAA CATTGCTTGA TGTTTCTTG TATGTCTACA TTAAACTTGA GAAAAAGTAA 2220
AAATTAGAAC ACTGTATGTA GTAATGAAAT TTCAGGGACC CAGAACATAA TGTAGTATAT 2280
GTTTTAGGT GGGAGATGCT GATAACAAAA TTAATAGGAA GTCTGTAGGC ATTAGGATAC 2340
TGACA 2345

(2) INFORMATION FOR SEQ ID NO: 147:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: PONSAZT01
(B) CLONE: 3057669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147 :

CCCACGCGTC CGCCCACGCG TCCGTTTCA GTAGGGATT CCTGTGACCA GACAAGTTCA 60
TCTGAGAGCC AGTTCTCACC ACTGGAATTC TCAGGAATGG ACCATGAGGA CATCAGTGAG 120
TCAGTGGATG CAGCATACAA CCTCCAGGAC AGTTGCCTTA CAGACTGTGA TGTGGAAGAT 180
GGGACTATGG ATGGCAATGA TGAGGGGCAC TCCTTGAAC TTTGTCCTTC TGAAGCTTCT 240
CCTTATGTAA GGTCAAGGGA GAGAACCTCC TCTTCAATAG TATTTGAAGA TTCTGGCTGT 300
GATAATGCTT CCAGTAAAGA AGAGCCGAAA ACTAATCGAT TGCATATTGG CAACCATTGT 360
GCTAATAAAC TAACTGCTTT CAAGCCCACC AGTAGCAAAT CTTCTCTGA AGCTACATTG 420
TCTATTCTC CTCCAAGACC AACCACTTTA AGTTTAGATC TCACTAAAAA CACCACAGAA 480

AAACTCCAGC CCAGTTCACC AAAGGTGTAT CTTTACATTC AAATGCAGCT GTGCAGAAA 540
GAAAACCTCA AAGACTGGAT GAATGGACGA TGTACCATAG AGGAGAGAGA GAGGAGCGTG 600
TGTCTGCACA TCTTCCTGCA GATCGCAGAG GCAGTGGAGT TTCTTCACAG TAAAGGACTG 660
ATGCACAGGG ACCTCAAGCC ATCCAACATA TTCTTTACAA TGGATGATGT GGTCAAGGTT 720
GGAGACTTTG GGTTAGTGAC TGCAATGGAC CAGGATGAGG AAGAGCAGAC GGTTCTGACC 780
CCAATGCCAG CTTATGCCAG ACACACAGGA CAAGTAGGGA CCAAACGTGTA TATGAGCCCA 840
GAGCAGATTG ATGGAAACAG CTATTCTCAT AAAGTGGACA TCTTTCTTT AGGCCTGATT 900
CTATTGAAAT TGCTGTATCC ATTCAGCACT CAGATGGAGA GAGTCAGGAC CTTAACTGAT 960
GTAAGAAATC TCAAATTCC ACCATTATT ACTCAGAAAT ATCCTGTGA GTACGTGATG 1020
GTTCAAGACA TGCTCTCTCC ATCCCCCATG GAACGACCTG AAGCTATAAA CATCATTGAA 1080
AATGCTGTAT TTGAGGACTT GGACTTTCCA GGAAAAACAG TGCTCAGACA GAGGTCTCGC 1140
TCCTTGAGTT CATCGGAAAC AAAACATTCA AGACAGTCCA ACAACTCCC TAGCCCTTG 1200
CCAAGCAATT AGCCTTAAGT TGTGCTAGCA ACCCTAATAG GTGATGCAGA TAATAGCCTA 1260
CTTCTTAGAA TATGCCGTGC CAAAATTGCA GACTTGAAAA GTTGTCTT CGCTCAATT 1320
TTTGTGGAC TACTTTTTT ATATCAAATT TAAGCTGGAT TTGGGGCAT AACCTAATT 1380
GAGCCAACTC CTGAGTTTG CTATACTTAA GGAAAGGGCT ATCTTGTTC TTTGTTAGTC 1440
TCTTGAAACT GGCTGCTGGC CAAGCTTAT AGCCCTCACC ATTTGCCTAA GGAGGTAGCA 1500
GCAATCCCTA ATATATATAT ATAGTGAGAA CTAAAATGGA TATTTTTA TAATGCAGAA 1560
GAAGGAAAGT CCCCCGTGT GGTAACTGTA TTGTTCTAGA AATATGCTTT CTAGAGATAT 1620
GATGATTTG AAAC TGATTT CTAGAAAAAG CTGACTCCAT TTTGTCCCT GGCGGGTAAA 1680
TTAGGAATCT GCACTATTT GGAGGACAAG TAGCACAAAC TGTATAACGG TTTATGTCCG 1740
TAGTTTATA GTCCTATTTG TAGCATTCAA TAGCTTTATT CCTTAGATGG TTCTAGGGTG 1800
GGTTTACAGC TTTTGTACT TTTACCTCCA ATAAAGGGAA AATGAAGCTT TTTATGTAAA 1860
TTGGTTGAAA GGTCTAGTT TGGGAGGAAA AAAGCCGTAG TAAGAAATGG ATCATATATA 1920
TTACAACCAA CTTCTCAAC TATGGACTTT TTAAGCCTAA TGAAATCTTA AGTGTCTTAT 1980
ATGTAATCCT GTAGGTTGGT ACTTCCCCCA AACTGATTAT AGGTAACAGT TTAATCATCT 2040
CACTTGCTAA CATGTTTTA TTTTCACTG TAAATATGTT TATGTTTAT TTATAAAAAT 2100
TCTGAAATCA ATCCATTGG GTGGTGGTG TACAGAACAC ACTTAAGTGT GTTAACTTGT 2160
GACTTCTTTC AAGTCTAAAT GATTTAATAA AACTTTTTT AAATTAAAAAA AAAAAA 2215

(2) INFORMATION FOR SEQ ID NO: 148:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: HEAONOT03
 - (B) CLONE: 3088178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148 :

GGTTGACATG ATGAACAATC GGTTTCGGAA GGATATGATG AAAAATGCTA GTGAAAGTAA 60
ACTTTCGAAA GACAACCTTA AAAAGAGACT TAAAGAAGAA TTCCAACATG CCATGGGAGG 120
AGTACCTGCC TGGGCAGAGA CTACTAACG GAAAACATCT TCAGATGATG AAAGTGAAGA 180
GGATGAAGAT GATTGTTGC AAAGGACTGG GAATTCATA TCCACATCAA CTTCTCTTCC 240
AAGAGGCATC TTGAAGATGA AGAACTGCCA GCATGCGAAT GCTGAACGTC CTACTGTTGC 300
TCGGATCTCA TCTGTGCAGT TCCATCCGG TGACAGATT GTGATGGTTG CTGGATTAGA 360
TAATGCTGTA TCACATTTC AGGTTGATGG GAAAACAAAT CCTAAAATTC AGAGCATCTA 420
TTTGGAAAGG TTTCCAATCT TTAAGGCTTG TTTTAGTGCT AATGGGAAG AAGTTTTAGC 480
CACGAGTACC CACAGCAAGG TTCTTATGT CTATGACATG CTGGCTGGAA AGTTAATTCC 540
TGTGCATCAA GTGAGAGGTT TGAAAGAGAA GATACTGAGG AGCTTGAAG TCTCCCCAGA 600
TGGGTCTTC TTGCTCATAA ATGGCATTGC TGGATATTG CATTGCTAG CAATGAAGAC 660
CAAAGAACTG ATTGGAAGCA TGAAAATTAA TGGAAGGGTT GCAGCATCCA CATTCTCTTC 720
AGATAGTAAG AAAGTATACG CCTCTTCGGG GGATGGAGAA GTTTATGTTT GGGATGTGAA 780
CTCAAGGAAG TGCCTTAACA GATTTGTTGA TGAAGGCAGT TTATATGGAT TAAGCATTGC 840
CACATCTAGG AATGGACAGT ATGTTGCTTG TGGTTCTAAT TGTGGAGTGG TAAATATATA 900
CAATCAAGAT TCTTGTCTCC AAGAAACAAA CCCAAAGCCA ATAAAAGCTA TAATGAACCT 960
GGTTACAGGT GTTACTTCTC TGACCTCAA TCCTACTACA GAAATCTTGG CAATTGCTTC 1020
AGAAAAAAATG AAAGAAGCAG TCAGATTGGT TCATCTTCCT TCCTGTACAG TATTTCAAA 1080
CTTCCCAGTC ATTAAAAATA AGAATATTTC TCATGTTCAT ACCATGGATT TTTCTCCGAG 1140
AAGTGGATAC TTTGCCTTGG GGAATGAAAA GGGCAAGGCC CTGATGTATA GGTTGCACCA 1200
TTACTCAGAC TTCTAAAGAG ACTATTTGAA GTCCAGTTGA GTCACAAGAG AAGCCTGTCT 1260
TGATATATCA TCTCAGAAC TTTCCTGAAT ATGTGATAAT ATATGGAAAA TGATTTATAG 1320
ATCCAGCTGT GCTTAAGAGC CAGTAATGTC TTAATAAACCA TGTGGCAGCT TTTGTTGAA 1380
AAAAAAAAAA AAAGG

1395

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2609 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT19
- (B) CLONE: 3094321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149 :

CCCGCCATGG CACTGTCGCG GGGGCTGCC CGGGAGCTGG CTGAGGCGGT GGCCGGGGC 60
CGGGTGCTGG TGGTGGGGC GGGCGGCATC GGCTGCGAGC TCCTCAAGAA TCTCGTGCTC 120
ACCGGTTTCT CCCACATCGA CCTGATTGAT CTGGATACTA TTGATGTAAG CAACCTCAAC 180
AGACAGTTT TGTTCAAAA GAAACATGTT GGAAGATCAA AGGCACAGGT TGCCAAGGAA 240
AGTGTACTGC AGTTTACCC GAAAGCTAAT ATCGTTGCCT ACCATGACAG CATCATGAAC 300
CCTGACTATA ATGTGGAATT TTTCCGACAG TTTATACTGG TTATGAATGC TTTAGATAAC 360
AGAGCTGCC GAAACCATGT TAATAGAATG TGCCTGGCAG CTGATGTTCC TCTTATTGAA 420
AGTGGAACAG CTGGGTATCT TGGACAAGTA ACTACTATCA AAAAGGGTGT GACCGAGTGT 480
TATGAGTGTGTC ATCCTAAGCC GACCCAGAGA ACCTTCCTG GCTGTACAAT TCGTAACACA 540
CCTTCAGAAC CTATACATTG CATCGTTGG GCAAAGTACT TGTCAACCA GTTGTGGGG 600
GAAGAAGATG CTGATCAAGA AGTATCTCCT GACAGAGCTG ACCCTGAAGC TGCCTGGGAA 660
CCAACGGAAG CGAAGCCAG AGCTAGAGCA TCTAATGAAG ATGGTGACAT TAAACGTATT 720
TCTACTAAGG AATGGGCTAA ATCAACTGGA TATGATCCAG TTAAACTTT TACCAAGCTT 780
TTTAAAGATG ACATCAGGTA TCTGTTGACA ATGGACAAAC TATGGCGGAA AAGGAAACCT 840
CCAGTTCCGT TGGACTGGC TGAAGTACAA AGTCAAGGAG AAGAAACGAA TGCATCAGAT 900
CAACAGAATG AACCCCAGTT AGGCCTGAAA GACCAGCAGG TTCTAGATGT AAAGAGCTAT 960
GCACGTCTTT TTTCAAAGAG CATCGAGACT TTGAGAGTTC ATTTAGCAGA AAAGGGGGAT 1020
GGAGCTGAGC TCATATGGGA TAAGGATGAC CCATCTGCAA TGGATTGT CACCTCTGCT 1080
GCAAACCTCA GGATGCATAT TTTCAGTATG AATATGAAGA GTAGATTGA TATCAAATCA 1140
ATGGCAGGGA ACATTATTCC TGCTATTGCT ACTACTAATG CAGTAATTGC TGGGTTGATA 1200
GTATTGGAAG GATTGAAGAT TTTATCAGGA AAAATAGACC AGTGCAGAAC AATTTTTTG 1260
AATAAACAAAC CAAACCCAAG AAAGAAGCTT CTTGTGCCTT GTGCACTGGA TCCTCCCAAC 1320

PF-0459 US

CCCAATTGTT ATGTATGTGC CAGCAAGCCA GAGGTGACTG TGC GGCTGAA TGTCCATAAA 1380
GTGACTGTTC TCACCTTACA AGACAAGATA GTGAAAGAAA AATTTGCTAT GGTAGCACCA 1440
GATGTCCAAA TTGAAGATGG GAAAGGAACA ATCCTAATAT CTTCCGAAGA GGGAGAGACG 1500
GAAGCTAATA ATCACAAAGAA GTTGTCAAGA TTTGGAATTAA GAAATGGCAG CCGGCTTCAA 1560
GCAGATGACT TCCTCCAGGA CTATACTTTA TTGATCAACA TCCTTCATAG TGAAGACCTA 1620
GGAAAGGACG TTGAATTGAG AGTTGTTGGT GATGCCCGG AAAAAGTGGG GCCCAAACAA 1680
GCTGAAGATG CTGCCAAAG CATAACCAAT GGCAGTGATG ATGGAGCTCA GCCCTCCACC 1740
TCCACAGCTC AAGAGCAAGA TGACGTTCTC ATAGTTGATT CGGATGAAGA AGATTCTTCA 1800
AATAATGCCG ACGTCAGTGA AGAAGAGAGA AGCCGCAAGA GGAAATTAGA TGAGAAAGAG 1860
AATCTCAGTG CAAAGAGGTC ACGTATAGAA CAGAAGGAAG AGCTTGATGA TGTCA TAGCA 1920
TTAGATTGAA CAGAAATGCC TCTAAACAGA ACCCTCTTAC TATTTAGTTT ATCTGGGCAG 1980
AACCAGATTG TTATGTCCTT TGTTCCAAAG GGAAAAAATT GACAGCAGTG ACTTGAAAAT 2040
GATTCTGCTC CCTTGAAAG CATTCACTTT GCTAGAACTG TTAGACACAT TGCAGTATGC 2100
TGTATTGAAA GTAGGAATAT AGTTTAAAA ACCCTTGAA CAAAGTGTGT GCATAACCAG 2160
TCATGAGATA AAACAACACA ATGCATGTTG CCTTTTAAT GTAAATACCC TTAGGTATCA 2220
TTAATAGTTT CAAAATATTG TGGTTAGTA AAGTTGATAC CTGGTTATAA ATATTATGCC 2280
TTTATTTTG GCTAGAAGAA GAATTATTT TAGCCTAGAT CTAACCATT TCATACTCTT 2340
AACTGATTGA AACAGATTCA AAGAAGTATC GAGTGCTATG CATTGAAACT TGTTTTAAA 2400
TGTTAGATGG CACTATGTAT ATTAATGTA AACAATGTTA ATTTACTCAA GTTTTCAGTT 2460
TGTACCGCCT GGTATGTCTG TGTAAGAAGC CAATTTTGT GTATTGTTAC AGTTTCAGGT 2520
TATTTATATT CGATGTTTG TAAAACCTCAA ATAACGACTA TACTTATGGA CCAAATAAAAT 2580
GGCATCTGCA TTCTGTTAA AAAAAAAA 2609

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3633 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: LUNGTUT13
(B) CLONE: 3115936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150 :

CCTGAGGGAT CCACAGAGGG TCGGGTCCTT GGAGGGAGGA CATGCAGTGC CACGTGCCAT 60
GGACCAGCCA GTGGACCCCA TGGCCAGCAA GGCTGCTCCT GGGGCCAGTG GGGTGGACAG 120
TCCCGCCAC GCAGGGTGAATG GAGGTGCCAG TGTGGGAATG AAAATGCGGC CTGTGCTCCT 180
GGGCCATGC GTCTCACGCT GCCCTTCCTC TCCAGGGAAAG CCTGTGTACC TGCTACTTT 240
TCCCGAACAA TTCATGGTAA AAACACAAAT GGTATATGGA CAAGATACTG AATGTGGAAG 300
AAACCTACTT GACAGTGTG GTGAAAATAG GGCCAGGATT TCACACCCGT GAATGCTTT 360
TACTGAAAAG TATTTGTGT TTTTCTCCCA GTTACAGAAAT GTCTGAAGGG GACAGTGTGG 420
GAGAATCCGT CCATGGGAAA CCTTCGGTGG TGTACAGATT TTTCACAAAGA CTTGGACAGA 480
TTTATCAGTC CTGGCTAGAC AAGTCCACAC CCTACACGGC TGTGCGATGG GTCGTGACAC 540
TGGGCCTGAG CTTGTCTAC ATGATTGAG TTTACCTGCT GCAGGGTTGG TACATTGTGA 600
CCTATGCCTT GGGGATCTAC CATCTAAATC TTTCATAGC TTTCTTTCT CCCAAAGTGG 660
ATCCTTCCTT AATGGAAGAC TCAGATGACG GTCCTTCGCT ACCCACCAAA CAGAACGAGG 720
AATTCCGCC CTTCATTGCA AGGCTCCAG AGTTAAATT TTGGCATGCG GCTACCAAGG 780
GCATCCTTGT GGCTATGGTC TGTACTTTCT TCGACGCTTT CAACGTCCCG GTGTTCTGGC 840
CGATTCTGGT GATGTACTTC ATCATGCTCT TCTGTATCAC GATGAAGAGG CAAATCAAGC 900
ACATGATTAA GTACCGGTAC ATCCCGTTCA CACATGGAA GAGAAGGTAC AGAGGCAAGG 960
AGGATGCCGG CAAGGCCTTC GCCAGCTAGA AGCGGGACTG AGGCTGCCTC ACGTGTGCA 1020
AGAACAGTT TGAGCCATTG TTAACAATGC CTTTTTCTT CACATAAAAGT AGTTGATTAC 1080
GAGGGAGTCA AATTTCTTT TTAAAAAGGA GCTTCAATGA TTTGTAACAG AAATATCAGG 1140
TTCTAGAAGA AACTGGCGCT TAAACCAAAT CGCATGGATT TCTTTTCAG TGACGTTCAA 1200
GTGTTCTCA CGGATGGAAT TCTAGTCAGC TGCAGGGCGGG AAGCCAGGCG GGTGGAGCCC 1260
ATGGGAGCAA GGGCGAGTGG CCGGTCCCCG CTGTGCCAGG TGGGCAGGCA GGAGCAAGGC 1320
CTGCGAGGGA GGAACGGGCC GCTCCCCGCC AGCCGCCTTC CCCAGCAGCC GCAGGTGGTG 1380
CCAGCCACTC CACAGAGCCC GAGGGATGAT CTAGCCTGAT TCCTGCGTGT CCGAAAGAAC 1440
TTAACGTTT AAAGGTGATT GTCAAGTAAC TGTGTGGGT TCTAATGCCA GTTTCCTAAT 1500
TCCATCTCAC TGGAGATGTT TAAAGTTGGC CTCTATCCTA ATGACTCAA ACTTGGTTCT 1560
TAACTACCAC GATTGCTTT GAGGGCCCGG AATTATAAAT ATATATTATA TTTAATTGT 1620
TTGAGATTAT TTTGACACAT TTCTTGATA CGTAGAGTGT TTTGTTTTA ATTTAAATCT 1680
GTCCTCATGC AACCCCTCCAT GAGGGGCAGC GAAGCTGGCA GGGAGCAGAC TGGCTTTGTA 1740
GGTTCAGCAC TCGGCCCCC ACTGCGGGAG AGGCAGAAC CACTTGCATG TCAGCGTTT 1800
TGATTGAGA AAAGAAATAC TCTCAACGTT TTACCAAGTG ATTTACCTC CACCTTACT 1860

AAAGTCTTA CCTAAAACAT GGCAGTCGCT GGACACAGGA AAGCCCACCT TTTGTTGGC 1920
 CTTTCGAAA GGTGACCCAT ATTGCACAGC AGAACATCAC AGCTGTGGTC CCAGATGAGA 1980
 CACTGACATG CGAGTGAAGG CCTCTCCTCC TGGGCCCCGG GCTGCCAGG CTCCTCACTC 2040
 TGGCGGTGT TTCTGTCTC AGAATTGACA CGGTGAATGC TTAGTGTCTG GATTTCTTG 2100
 TGCCAGTGT TACATATCTG ACATCGAGCT CCTCTAAGAG GCCACGTTCA AGCTTGTGTG 2160
 TCCCTGACCC AAGATAGCCA GTGCTGCTCC CAGGTGGTAC TTCTGGTACC GTGTTGAGAC 2220
 ACTTGGGATT CTCAGACTGT GGACAGGGAGT GTTTGTCATT TTTCATACTG TTTTCTTAAT 2280
 AAGCGCTCAG GCCTAAGGTG TGACAGGAAG TCGCACGCGC TTGGCCAGAG CACAGTGAAG 2340
 CAAAGGACTG GGTGCTGATG GATGGAGCCA CGGGCGCATC TGCCCACCCG GCCGCAGCCC 2400
 CCAGTGCCTC TCCTGGTGGT CCTCCCAGTC TAGAGGGTCA CGGCCCCCCC GCCCTCCTCC 2460
 GTCTCTGGCA AGCTGACCTT GACTAACCCA GGAATACAGG GTCATCCTCA TTCCTAAGTA 2520
 AGTCAAACAG CAAGACATGG TTTGCGCGGG TCTTGCCGG AAGCCGGTCC TGCTGGCCAG 2580
 GTGTTTACG TCAGCAGGGA AATGTGGCAC ACGCCCTCGA GGCATTTAA CACTGTGCTT 2640
 CAGGAAATCT CAAGTTCCAT CTTGTGTTAG TAACGTACCC ACATTTGCT GGAGTTAGTT 2700
 TATTAAAGAT GCCTACGGTG AACTCTCTGG CGCAGGTTAA ATGCAGTTT GAAAACCTGG 2760
 AAACATCAA TGGAGGCGGG AAATAGGCTG GGGCCGAGCT GAGGGGCTGA ACACAGCAGT 2820
 GACCGTGGGT CAGCAGGTG CCTGCCAGC AGGCCCCCA GGAGAGGGCT CGGGCGCCCC 2880
 TGGCAGCCCC CATACCCCCA GGACCTGGCT CGTGAGTGC TCTGGTCAG GAAGAGACCT 2940
 CTCTGTGCGT CTCAGGCTGA GATGCAGATT TCTGTTTCT AAAACTGGAA GCGACCTTGA 3000
 CGTGTATTGA AGGTGTGTGT GCCAAATGCT TCCGACGGAG GTGCTGGCCT TGGTTGGTT 3060
 CTCTCTGCC CGTGTGGTCA TCAAGTCCTG GGGGATGTGC TCTGCCAGC CGCCCTCGGG 3120
 GAGAGCAGCG CGCCTCCCA TGGGGCCGTG GGGCTGCTGT TCTCACTGCA CTGGCTGAAG 3180
 CAACCCGCCA GCCTCCGTGC CCCACCCAC CCAGCACGCA CTCATTCACT CCATTGCCCT 3240
 AACACAAGCC TGATGGGCT GTTTCTCAC AATATAAACG AATAAAGTGT CTTCTGGCCT 3300
 ACTTCTGAAT TACTTCTCAA CTGTATGGTT TGGGAAAGGG AGGGAAACCT AAAATCCCGT 3360
 CCAAATAAGT GAAATTCCCTG AAGAAGTGGC TGAGTCCTAC CAGGTTGGGG TTAGGGAAAT 3420
 GTTCTGGGTT CAGGCGCCCC TCCCAGGGCT GAGAAAGCGC AGCCAGGGAC AGCTTCTGT 3480
 TCTCTCCAG GGTGGCTAGG TTAGTATCTT ACATGACAAA AAACTGAGAG TGTTCTAACT 3540
 TCTGTGCAAG CAAGGTTAAT CCTGAGACTA AATCTTGGCG TTCAGACTCC CGTAGAGGTC 3600
 ATCTGTGTCC AGGCCCACCC GGGCGCCGGC TCA 3633

(2) INFORMATION FOR SEQ ID NO: 151:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2018 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: LUNGTUT13
 - (B) CLONE: 3116522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151 :

TGGCTCGCTG GCCGCTCCTG GAGGCGCGG CGGGAGCGCA GGGGGCGCGC GGCCCGGGA 60
CTCGCATTCC CCGGTTCCCC CTCCACCCCA CGCGGCCTGG ACCATGGACG CCAGATGGTG 120
GGCAGTGGTG GTGCTGGCTG CGTTCCCCTC CCTAGGGGCA GGTGGGGAGA CTCCCGAAGC 180
CCCTCCGGAG TCATGGACCC AGCTATGGTT CTTCCGATTT GTGGTGAATG CTGCTGGCTA 240
TGCCAGCTTT ATGGTACCTG GCTACCTCCT GGTGCAGTAC TTCAGGCGGA AGAACTACCT 300
GGAGACCGGT AGGGGCCTCT GCTTCCCCCT GGTGAAAGCT TGTGTGTTG GCAATGAGCC 360
CAAGGCCTCT GATGAGGTTC CCCTGGCGCC CCGAACAGAG GCGGCAGAGA CCACCCCGAT 420
GTGGCAGGCC CTGAAGCTGC TCTTCTGTGC CACAGGGCTC CAGGTGTCTT ATCTGACTTG 480
GGGTGTGCTG CAGGAAAGAG TGATGACCCG CAGCTATGGG GCCACAGCCA CATCACCGGG 540
TGAGCGCTTT ACGGACTCGC AGTTCTGGT GCTAATGAAC CGAGTGCTGG CACTGATTGT 600
GGCTGGCCTC TCCTGTGTT CTCGAAGCA GCCCCGGCAT GGGGCACCCA TGTACCGGTA 660
CTCCTTGCC AGCCTGTCCA ATGTGCTTAG CAGCTGGTGC CAATACGAAG CTCTTAAGTT 720
CGTCAGCTTC CCCACCCAGG TGCTGGCAA GCCCTCTAAG GTGATCCCTG TCATGCTGAT 780
GGGAAAGCTT GTGTCTCGC GCAGCTACGA ACACTGGGAG TACCTGACAG CCACCCCTCAT 840
CTCCATTGGG GTCAGCATGT TTCTGCTATC CAGCGGACCA GAGCCCCGCA GCTCCCCAGC 900
CACCACACTC TCAGGCCTCA TCTTACTGGC AGGTTATATT GCTTTGACA GCTTCACCTC 960
AAACTGGCAG GATGCCCTGT TTGCCTATAA GATGTCATCG GTGCAGATGA TGTTGGGGT 1020
CAATTCTTC TCCTGCCTCT TCACAGTGGG CTCACTGCTA GAACAGGGGG CCCTACTGGA 1080
GGGAACCCGC TTCATGGGGC GACACAGTGA GTTGCTGCC CATGCCCTGC TACTCTCCAT 1140
CTGCTCCGCA TGTGCCAGC TCTTCATCTT TTACACCATT GGGCAGTTG GGGCTGCCGT 1200
CTTCACCACATC ATCATGACCC TCCGCCAGGC CTTGCCATC CTTCTTCCT GCCTTCTCTA 1260
TGGCCACACT GTCACTGTGG TGGGAGGGCT GGGGGTGGCT GTGGTCTTG CTGCCCTCCT 1320
GCTCAGAGTC TACGCGCGGG GCCGTCTAAA GCAACGGGGA AAGAAGGCTG TGCCTGTTGA 1380

GTCTCCTGTG CAGAAGGTTT GAGGGTGGAA AGGGCCTGAG GGGTGAAGTG AAATAGGACC 1440
 CTCCCACCAT CCCCTCTGC TGTAACCTCT GAGGGAGCTG GCTGAAAGGG CAAAATGCAG 1500
 GTGTTTCTC AGTATCACAG ACCAGCTCTG CAGCAGGGGA TTGGGGAGCC CAGGAGGCAG 1560
 CCTTCCCTTT TGCCTTAAGT CACCCATCTT CCAGTAAGCA GTTTATTCTG AGCCCCGGGG 1620
 GTAGACAGTC CTCAGTGAGG GGTTTGGGG AGTTTGGGT CAAGAGAGCA TAGGTAGGTT 1680
 CCACAGTTAC TCTTCCACA AGTCCCTTA AGTCTGCCC TAGCTGTGCT CTGCCACCTT 1740
 CCAGACTCAC TCCCCCTGC AAATACCTGC ATTTCTTACC CTGGTGAGAA AAGCACAAGC 1800
 GGTGTAGGCT CCAATGCTGC TTTCCCAGGA GGGTGAAGAT GGTGCTGTGC TGAGGAAAGG 1860
 GGATGCAGAG CCCTGCCAG CACCACCACC TCCTATGCTC CTGGATCCCT AGGCTCTGTT 1920
 CCATGAGCCT GTTGCAAGGTT TTGGTACTTT AGAAATGTAA CTTTTGCTC TTATAATT 1980
 ATTTTATTAA ATAAATTAC TGCAAGTGAA AAAAAAAA 2018

0
 9
 8
 7
 6
 5
 4
 3
 2
 1

(2) INFORMATION FOR SEQ ID NO: 152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 942 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: LUNGUT13
 - (B) CLONE: 3117184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152 :

CCTCCATCAG CTCGCCGCAG AGCGGCTGTA TTTGCGGCCT GTGCGAGTAG GCGCTTGGGC 60
 ACTCAGTCTC CCTGGCGGGC GACGGGCAGA AATCTCGAAC CAGTGGAGCG CACTCGTAAC 120
 CTGGATCCCA GAAGGTCGCG AAGGCAGTAC CGTTTCTCA GCGGCGGACT GCTGCAGTAA 180
 GAATGTCTT TCCACCTCAT TTGAATCGCC CTCCCATGGG AATCCCAGCA CTCCCACCAG 240
 GGACCCCACC CCCGCAGTTT CCAGGATTT CTCCACCTGT ACCTCCAGGG ACCCCAAATGA 300
 TTCCGTACCC AATGAGCATT ATGGCTCCTG CTCCGACTGT CTTAGTACCC ACTGTGTCTA 360
 TGGTTGGAAA GCATTTGGGC GCAAGAAAGG ATCATCCAGG CTTAAAGGCT AAAGAAAATG 420
 ATGAAAATTG TGGCCTACT ACCACTGTTT TTGTTGGCAA CATTTCGAG AAAGCTTCAG 480
 ACATGCTTAT AAGACAACTC TTAGCTAAAT GTGGTTGGGT TTTGAGCTGG AAGAGAGTAC 540
 AAGGTGCTTC CGGAAAGCTT CAAGCCTTCG GATTCTGTGA GTACAAGGAG CCAGAATCTA 600
 CCCTCCGTGC ACTCAGATTA TTACATGACC TGCAAATTGG AGAGAAAAAG CTACTCGTTA 660

AAGTTGATGC AAAGACAAAG GCACAGCTGG ATGAATGGAA AGCAAAGAAG AAAGCTTCTA 720
ATGGGAATGC AAGGCCAGAA ACTGTCACTA ATGACGATGA AGAACCTTG GATGAAGAAA 780
CAAAGAGGAG AGATCAGATG ATTAAAGGGG CTATTGAAGT TTTAATTCTG GAATACTCCA 840
GTGAGCTAAA TGCCCCCTCA CAGGAATCTG ATTCTCACCC CAGGAAGAAG AAGAAGGAAA 900
AGAAGGAGGA CATTTCGGC AGATTTCACTG GGGCCCACGT AT 942

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2060 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LNODNOT05
- (B) CLONE: 3125156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153 :

TCCCCCCCCTC AGCCTCCCCC CCCCCCACTG GCATATGGTC CTGCCCCCTTC TACCAGACCC 60
ATGGGCCCCC AGGCAGCCCC TCTTACCAATT CGAGGGCCCT CGTCTGCTGG CCAGTCCACC 120
CCTAGTCCCC ACCTGGTGCC TTCACCTGCC CCATCTCCAG GGCCTGGTCC GGTACCCCCT 180
CGCCCCCCCAG CAGCAGAACCC ACCCCCCTGC CTGCGCCGAG GCGCCGCAGC TGCAGACCTG 240
CTCTCCTCCA GCCCGGAGAG CCAGCATGGC GGCACTCAGT CTCCTGGGGG TGGGCAGCCC 300
CTGCTGCAGC CCACCAAGGT GGATGCAGCT GAGGGTCGTC GGCCGCAGGC CCTGCGGCTG 360
ATTGAGCGGG ACCCCATATGA GCATCCTGAG AGGCTGCGGC AGTTGCAGCA GGAGCTGGAG 420
GCCTTCGGG GTCAGCTGGG GGATGTGGGA GCTCTGGACA CTGTCTGGCG AGAGCTGCAA 480
GATGCGCAGG AACATGATGC CCGAGGCCGT TCCATGCCA TTGCCCGCTG CTACTCACTG 540
AAGAACCGGC ACCAGGATGT CATGCCCTAT GACAGTAACC GTGTGGTGT GCGCTCAGGC 600
AAGGATGACT ACATCAATGC CAGCTGCGTG GAGGGCTCT CCCCATACTG CCCCCCGCTA 660
GTGGCAACCC AGGCCCACT GCCTGGCACA GCTGCTGACT TCTGGCTCAT GGTCCATGAG 720
CAGAAAGTGT CAGTCATTGT CATGCTGGTT TCTGAGGCTG AGATGGAGAA GCAAAAGTG 780
GCACGCTACT TCCCCACCGA GAGGGGCCAG CCCATGGTGC ACGGTGCCCT GAGCCTGGCA 840
TTGAGCAGCG TCCGCAGCAC CGAAACCCAT GTGGAGCGCG TGCTGAGCCT GCAGTTCCGA 900
GACCAGAGCC TCAAGCGCTC TCTTGTGCAC CTGCACTTCC CCACTTGGCC TGAGTTAGGC 960
CTGCCCGACA GCCCCAGCAA CTTGCTGCGC TTCACTCCAGG AGGTGCACGC ACATTACCTG 1020

PF-0459 US

CATCAGCGGC CGCTGCACAC GCCCATCATT GTGCACTGCA GCTCTGGTGT GGGCCGCACG 1080
GGAGCCTTG CACTGCTCTA TGCAGCTGTG CAGGAGGTGG AGGCTGGAA CGGAATCCCT 1140
GAGCTGCCTC AGCTGGTGCG GCGCATGCGG CACGAGAGAA AGCACATGCT GCAGGAGAAG 1200
CTGCACCTCA GGTTCTGCTA TGAGGCAGTG GTGAGACACG TGGAGCAGGT CCTGCAGCGC 1260
CATGGTGTGC CTCCTCCATG CAAACCCCTG GCCAGTGCAA GCATCAGCCA GAAGAACAC 1320
CTTCCTCAGG ACTCCCAGGA CCTGGTCCTC GGTGGGGATG TGCCCATCAG CTCCATCCAG 1380
GCCACCATTG CCAAGCTCAG CATTGGCCT CCTGGGGGGT TGGAGTCCCC GGTTGCCAGC 1440
TTGCCAGGCC CTGCAGAGCC CCCAGGCCTC CGGCCAGCCA GCCTCCCAGA GTCTACCCCA 1500
ATCCCATCTT CCTCCCAAAC CCCCTTCCTT CCCCACCTACC TGAGGCTCCC CAGCCTAAGG 1560
AGGAGCCGCC AGTGCCTGAA GCCCCCAGCT CGGGGCCCCC CTCCCTCCTCC CTGGAATTGC 1620
TGGCCTCCTT GACCCAGAG GCCTTCTCCC TGGACAGCTC CCTGCGGGGC AACACAGCGGA 1680
TGAGCAAGCA TAACTTTCTG CAGGCCATA ACAGGGCAAGG GCTGCGGCC ACCCGGCCCT 1740
CTGACGACCC CCTCAGCCTT CTGGATCCAC TCTGGACACT CAACAAGACC TGAACAGGTT 1800
TTGCCTACCT GGTCTTACA CTACATCATC ATCATCTCAT GCCCACCTGC CCACACCCAG 1860
CAGAGCTTCT CAGTGGCAG AGTCTTTAC TCCCATTCT GCTGCCTTG GCCCTGCCTG 1920
GCCCAGCCTG CACCCCTGTG GGGTGGAAAT GTACTGCAGG CTCTGGTCA GGTTCTGCTC 1980
CTTTATGGGA CCCGACATTT TTCAGCTCTT TGCTATTGAA ATAATAAACC ACCCTGTTCT 2040
GTGAAAAAAA AAAAAAAAAG 2060

(2) INFORMATION FOR SEQ ID NO: 154:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2065 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: LUNGUT12
 - (B) CLONE: 3129120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154 :

CGGGTCCCCG GGTCTGACAG GAGCAGCCTG TGGGCACCGC GGCGGTAGTT GGAGGCAGGA 60
GAGGGTCCGT AGCCCGCGCG CCCTGCCCG CCATGGGCCT CCTGTCGGAC CCGGTTGCC 120
GGCGCGCGCT CGCCCGCTA GTGCTGCGCC TCAACGCGCC GTTGTGCGTG CTGAGCTACG 180
TGGCGGGCAT CGCCTGGTTC TTGGCGCTGG TTTTCCCGCC GCTGACCCAG CGCACTTACA 240

TGTCGGAGAA CGCCATGGC TCCACCATGG TGGAGGAGCA GTTTGCGGGC GGAGACCGTG 300
CCCGGGCTTT TGCCCGGGAC TTGCGCGCCC ACCGCAAGAA GTCGGGGCT CTGCCAGTGG 360
CCTGGCTTGA ACGGACGATG CGGTCACTAG GGCTGGAGGT CTACACGCAG AGTTTCTCCC 420
GGAAACTGCC CTTCCCAGAT GAGACCCACG AGCGCTATAT GGTGTCGGC ACCAACGTGT 480
ACGGCATTCT GCAGGGCCCCG CGTGCCTGCCA GCACCGAGTC GCTTGTGCTC ACCGTGCCCT 540
GTGGCTCTGA CTCTACCAAC AGCCAGGCTG TGGGGCTGCT GCTGGCACTG GCTGCCCACT 600
TCCGGGGGCA GATTATTGG GCCAAAGATA TCGTCTTCCT GGTAACAGAA CATGACCTTC 660
TGGGCAGTGA GGCTTGGCTT GAAGCCTACC ACGATGTCAA TGTCACTGGC ATGCAGTCGT 720
CTCCCCCTGCA GGGCCGAGCT GGGGCCATTC AGGCAGCCGT GGCCCTGGAG CTGAGCAGTG 780
ATGTGGTCAC CAGCCTCGAT GTGGCCGTGG AGGGGCTTAA CGGGCAGCTG CCCAACCTTG 840
ACCTGCTCAA TCTCTTCCAG ACCTTCTGCC AGAAAGGGGG CCTGTTGTGC ACGTTCAAGG 900
GCAAGCTGCA GCCCGAGGAC TGGACATCAT TGGATGGACC GCTGCAGGGC CTGCAGACAC 960
TGCTGCTCAT GGTTCTGCGG CAGGCCTCCG GCCGCCCTCA CGGCTCCCAT GGCTCTTCC 1020
TGCCTACCG TGTGGAGGCC CTAACCCCTGC GTGGCATCAA TAGCTTCCGC CAGTACAAGT 1080
ATGACCTGGT GGCAGTGGGC AAGGCTTGG AGGGCATGTT CCGCAAGCTC AACACACCTCC 1140
TGGAGCGCCT GCACCAGTCC TTCTTCCCT ACTTGCTCCC CGGCCTCTCC CGCTTCGTCT 1200
CCATCGGCCT CTACATGCC GCTGTCGGCT TCTTGCTCCT GGTCTTGTT CTCAAGGCTC 1260
TGGAACTGTG GATGCAGCTG CATGAGGCTG GAATGGGCCT TGAGGAGCCC GGGGGTGCCTC 1320
CTGGCCCCAG TGTACCCCTT CCCCCATCAC AGGGTGTGGG GCTGGCCTCG CTCGTGGCAC 1380
CTCTGCTGAT CTCACAGGCC ATGGGACTGG CCCTCTATGT CCTGCCAGTG CTGGGCCAAC 1440
ACGTTGCCAC CCAGCACTTC CCAGTGGCAG AGGCTGAGGC TGTGGTGCTG ACACTGCTGG 1500
CGATTTATGC AGCTGGCCTG GCCCTGCCCA ACAATACCCA CCGGGTGGTA AGCACACAGG 1560
CCCCAGACAG GGGCTGGATG GCACTGAAGC TGGTAGCCCT GATCTACCTA GCACTGCAGC 1620
TGGGCTGCAT CGCCCTCAC AACTTCTCAC TGGGCTTCCCT GCTGGCCACC ACCATGGTGC 1680
CCACTGCTGC GCTTGCCAAG CCTCATGGC CCCGGACCCCT CTATGCTGCC CTGCTGGTGC 1740
TGACCAGCCC GGCAGCCACG CTCCTGGCA GCCTGTTCCCT GTGGCGGGAG CTGCAGGAGG 1800
CGCCACTGTC ACTGGCCGAG GGCTGGCAGC TCTTCCTGGC AGCGCTAGCC CAGGGTGTGC 1860
TGGAGCACCA CACCTACGGC GCCCTGCTCT TCCCAGTGCT GTCCCTGGC CTCTACCCCT 1920
GCTGGCTGCT TTTCTGGAAT GTGCTCTTCT GGAAGTGAGA TCTGCCTGTC CGGGCTGGGA 1980
CAGAGACTCC CCAAGGACCC CATTCTGCC CTTCTGGGG AAATAAATGA GTGTCTGTTT 2040
CAGCAGCTAT TTGATGCTTG TCACA

2065